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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 90 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-3
Perfect score: 172
Sequence: 1 USELDDRADALQAXASQPEXSAKLKRWKGNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	169	98.3	37	2	AAR6822 VAMP iso1
2	169	98.3	40	4	AAB50301 VAMP2 pep
3	169	98.3	40	4	AAB48582 VAMP2 pep
4	169	98.3	42	5	AA015163 Clostridi
5	169	98.3	54	3	AAB39482 Gene 49 h
6	169	98.3	62	2	AAR6821 VAMP iso1
7	169	98.3	115	7	ADE57598 Human Pro
8	169	98.3	115	7	ADE57612 Rat Prote
9	169	98.3	115	7	ADE60831 Human Pro
10	169	98.3	115	7	ADE57606 Human Pro
11	169	98.3	115	7	ADE60829 Rat Prote
12	169	98.3	115	7	ADE57600 Rat Prote
13	169	98.3	115	7	ADE57604 Rat Prote
14	169	98.3	115	7	ADE57596 Rat Prote
15	169	98.3	115	7	ADE57602 Human Pro
16	169	98.3	115	7	ADE57610 Human Pro
17	169	98.3	115	7	ADE57592 Rat Prote
18	169	98.3	115	7	ADE57594 Human Pro
19	169	98.3	115	7	ADE57614 Human Pro
20	169	98.3	115	7	ADE57608 Rat Prote
21	169	98.3	116	2	AAW30104 Vesicle-a
22	169	98.3	116	2	AAW43425 Rat Vesic
23	169	98.3	116	3	AAV88243 Bovine sy
24	169	98.3	116	5	ABP43681 VAMP-2 se
25	169	98.3	116	6	ABP76220 Human GEN

26	169	98.3	116	6	AAE36664 Human VAM
27	169	98.3	116	7	ABW01719 Bovine VA
28	169	98.3	116	7	ABW01718 Mouse VAM
29	169	98.3	116	7	ABW01705 Human VAM
30	169	98.3	116	7	ADG89011 Bovine sy
31	169	98.3	116	8	ADM97006 Mouse VAM
32	169	98.3	116	8	ADM97007 Bovine VA
33	169	98.3	116	8	ADM97005 Human VAM
34	169	98.3	368	3	AAV43843 Rat VAMP
35	169	98.3	368	3	ADP90403 Rat VAMP
36	169	98.3	608	3	AAV43845 Rat VAMP
37	169	98.3	609	7	ADP90406 Rat VAMP
38	167	97.1	35	5	AA015157 Clostridi
39	167	97.1	82	3	AAV88244 Xenopus s
40	167	97.1	82	7	ADG89012 Frog VAMP
41	167	97.1	114	7	ABW01720 Frog VAMP
42	167	97.1	114	8	ADM97008 Frog VAMP
43	164	95.3	35	2	AAR6824 VAMP iso1
44	164	95.3	100	2	AAW04182 Cellulose
45	164	95.3	100	3	AAV88240 Human cel

ALIGNMENTS

RESULT 1	AAE36664	standard; peptide: 37 AA.
ID	AAE36664	
XX	AAE36664	
AC	AAE36664	
XX	AAE36664	
DT	15-AUG-1996	(first entry)
XX	15-AUG-1996	
DE	VAMP isoform-1 residues 60-94	(plus N- and C-terminal cysteines).
XX	VAMP; vesicle-associated membrane protein; SNF-25; syntaxin;	
KW	neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;	
KW	antibody; detection; assay.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 1	/label= N-terminal Cysteine
FT	Peptide	/note= "may be present to attach peptide to solid-phase"
FT	Peptide	2..36
FT	Misc-difference 37	/note= "VAMP isoform-1 residues 60-94"
FT	Misc-difference 37	/label= C-terminal cysteine
FT	Misc-difference 37	/note= "may be present to attach to peptide to solid-phase"
XX	WO9533850-A1.	
PN	14-DEC-1995.	
XX	02-JUN-1995;	95WO-GB001279.
XX	03-JUN-1994;	94GB-00011138.
PR		
XX		
PA	(MICR-) MICROBIOLOGICAL RES AUTHORITY.	
XX	(CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.	
PI	Shore CC, Hallis B, Tames BAF, Quinn CP;	
XX	WPI; 1996-040249/04.	
XX	Assay for botulinum or tetanus toxin - by combining test cpd. with	
PT	substrate which is cleaved by the toxin, and antibody specific for the	
PT	cleaved but not uncleaved substrate.	
XX		
PS	Example 1; Page 28-29; 48pp; English.	
XX		

CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
 CC activities within their light sub-units. Depending on the neurotoxin type
 CC these act to cleave small proteins within the nerve cell which are
 CC involved in neurotransmitter release. Antibodies are used in assays which
 CC detect cleaved but not uncleaved substrate. An assay for botulinum type B
 CC uses the present sequence as a substrate. It is VAMP (vesicle-associated
 CC membrane protein) isoform-1, residues 60-94. The VAMP peptide can be
 CC attached by a C- or N-terminal cysteine to a solid phase
 CC
 XX

SQ Sequence 37 AA;

Query Match 98.3%; Score 169; DB 2; Length 37;
 Best Local Similarity 94.3%; Pred. No. 7, 2e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 DB 2 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 36

RESULT 2

ID AAB50301 standard; peptide; 40 AA.

AC AAB50301;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

KW VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;
 KM tetanus neurotoxin; buforinin.

OS Unidentified.

XX MO200069891-A2.

PD 23-NOV-2000.

PF 15-MAY-2000; 2000WO-US013215.

PR 17-MAY-1999; 99US-0134446P.

XX (USSA) US DEPT OF THE ARMY.

PA Gordon RK, Moorad DR, Doctor BP, Garcia GE;

PI WPI; 2001-025001/03.

DR Novel Previn compounds useful for inhibiting the protease activity of
 PT Botulinum B and tetanus toxins.

PS Disclosure; Page 5; 47pp; English.

CC The present sequence was investigated in the search for Botulinum toxin
 CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity
 CC of BttxB and tetanus neurotoxins were isolated. Previns may be used to
 CC construct compounds such as buforinins
 CC
 XX

SQ Sequence 40 AA;

Query Match 98.3%; Score 169; DB 4; Length 40;
 Best Local Similarity 94.3%; Pred. No. 7, 2e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 DB 6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40

RESULT 3

ID AAB48582 standard; peptide; 40 AA.

XX AAB48582;
 AC 08-MAR-2001 (first entry)
 DT VAMP2 peptide.
 DE Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;
 XX antibacterial; VAMP2; synaptobrevin.
 KM
 XX

OS Unidentified.
 XX
 XX MO200069895-A2.
 PN
 XX
 XX 23-NOV-2000.
 PD

PF 11-MAY-2000; 2000WO-US012909.

PR 14-MAY-1999; 99US-0134216P.

XX (USSA) US DEPT OF THE ARMY.

PA Garcia GE, Gordon RK, Moorad DR, Doctor BP;

PI WPI; 2001-102250/11.

DR Novel peptides capable of inhibiting the enzymatic activity of Botulinum
 PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic
 PT poisoning such as Botulinum toxin and tetanus poisoning.
 XX

PS Disclosure; Page 5; 47pp; English.

CC The present sequence is one of a number of peptide or peptide-like
 CC compounds, designated buforinins, which inhibit the enzymatic activity of
 CC Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforinins are
 CC useful for treating Botulinum or tetanus intoxication by administering a
 CC composition comprising a buforin to the subject prior to the contact with
 CC BttxB or tetanus intoxication. Antibodies specific for buforins are
 CC useful for detecting buforins by forming immunocomplexes. The buforins
 CC have improved circulatory half-life, solubility, resistance to
 CC degradation and interaction with the active site of the toxin
 CC
 XX

SQ Sequence 40 AA;

Query Match 98.3%; Score 169; DB 4; Length 40;
 Best Local Similarity 94.3%; Pred. No. 7, 2e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 DB 6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40

RESULT 4

AAO15163 standard; peptide; 42 AA.

XX AAO15163;

AC 02-SEP-2002 (first entry)

DT Clostridial neurotoxin protease substrate peptide 2.

DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;

KW fluorescence resonant energy transfer assay; quenched-signal;

KM clostridial neurotoxin detection; food.

XX Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-fluoresceinyl-L-glycine"
 FT Cleavage-site 20..21

/note= "The peptide is cleaved between these two residues
by the clostridial neurotoxin"

WO200225284-A2.

28-MAR-2002.

25-SEP-2001; 2001WO-US030188.

25-SEP-2000; 2000US-0235050P.

(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

Schmidt JT, Stafford RG;

WPI; 2002-499829/53.

Substrate useful in e.g. an assay for the protease activity of
clostridial neurotoxin, comprises modified peptide or protein.

Claim 24; Page 15; 48pp; English.

The invention comprises clostridial neurotoxin substrate peptides which
can serve as fluorescence resonant energy transfer assay (FRET) or
quenched-signal substrates in assays for the proteolytic activities of
clostridial neurotoxins. The invention further comprises clostridium
botulinum neurotoxin substrate peptides that can serve as immobilised
substrates (i.e. bound to a solid phase) in assays for the proteolytic
activities of clostridial neurotoxins. The clostridial (including the
Clostridium botulinum) neurotoxin substrate peptides are useful for
detecting the presence of clostridial neurotoxins in a sample (e.g. food
or an environmental sample). The present amino acid sequence represents a
clostridial neurotoxin substrate peptide of the invention

Sequence 42 AA;

Query Match 98.3%; Score 169; DB 5; Length 42;
Best Local Similarity 94.3%; Pred. No. 7.6e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSEIDDRADALQAXASQFEXSAKLKRYWKXK 35

DB 4 LSEIDDRADALQAGASQFETSAKLKRYWKXK 38

RESULT 5
AAB39482
ID AAB39482 standard; protein; 54 AA.

AAB39482;

02-FEB-2001 (first entry)

Gene 49 human secreted protein homologous amino acid sequence #111.

Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
neurotropic; neuroprotection; antiviral; antiallergic; hepatotropic;
antidiabetic; antiinflammatory; antitumor; anticonvulsant;
antibacterial; antifungal; antiparasitic; cardiac; gene therapy;
food additive; preservative; chromosome identification; cancer;
female reproductive system disorder; immune disorder; wound healing;
cardiovascular disorder; neurological disease; infectious disease;
infection.

Bos taurus.

WO200058340-A2.

05-OCT-2000.

23-MAR-2000; 2000WO-US007724.

26-MAR-1999; 99US-0126510P

07-JAN-2000; 2000US-0174850P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM, Komatsoulis G;

WPI; 2000-594638/56.

Fifty nucleic acid molecules encoding human secreted proteins, useful in
the prevention, treatment and diagnosis of cancer, immune disorders,
cardiovascular disorders and neurological diseases.

Disclosure; Page 390; 391pp; English.

The polynucleotide sequences given in AAC74337 to AAC74386 encode the
human secreted proteins given in AAB39402 to AAB39451. AAB39452 to
AAB39484 represent human secreted polypeptide sequences and proteins
homologous to them, which are given in the exemplification of the present
invention. Human secreted proteins have activities based on the tissues
and cells the genes are expressed in. Example of activities include:
cytostatic; immunosuppressive; neurotropic; neuroprotection; antiviral;
antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
cardiac. The polynucleotides and polypeptides are useful for preventing,
treating or ameliorating a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
can also be used as a food additive or preservative to increase or
decrease storage capabilities. The polynucleotide are useful for
chromosome identification. They are also useful as probes for diagnosing
a disorder related to the female reproductive system, particularly breast
and/or ovarian cancer. They are also useful in the gene therapy of breast
and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,
agonists and antagonists are useful in the diagnosis, treatment and
prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular
disorders; (d) wound healing; (e) neurological diseases; and (f)
infectious diseases such as viral, bacterial, fungal and parasitic
infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in
the exemplification of the present invention

Sequence 54 AA;

Query Match 98.3%; Score 169; DB 3; Length 54;
Best Local Similarity 94.3%; Pred. No. 1e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSEIDDRADALQAXASQFEXSAKLKRYWKXK 35

DB 20 LSEIDDRADALQAGASQFETSAKLKRYWKXK 54

RESULT 6
AAB86821
ID AAB86821 standard; peptide; 62 AA.

AAB86821;

15-AUG-1996 (first entry)

VAMP isoform-1 residues 33-94.

VAMP, vesicle-associated membrane protein; SNAP-25; syntaxin;
neurotransmitter; neurotoxin; botulinum; botulinum; cleavage; substrate;
antibody; detection; assay.

Synthetic.

WO9533850-A1.

14-DEC-1995.

02-JUN-1995; 95WO-GB001279.

03-JUN-1994; 94GB-00011138.

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX WPI, 1996-040249/04.
XX
XX Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
XX Example 3; Page 28; 48pp; English.
XX
XX The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the
CC protein VAMP (vesicle-associated membrane protein) at an identical site
CC to that of botulinum toxin type B (BONT/B). The specificities of the
CC endopeptidase activities of the two toxins however differ in the minimum
CC peptide substrate size required for cleavage. While BONT/B requires
CC peptide substrates of 30-35 residues in length for optimal cleavage, the
CC requirement for tetanus toxin is peptide substrates of >50 residues in
CC length. The present sequence, VAMP isoform-1 residues 33-94, is a
CC suitable substrate for tetanus toxin
XX
SQ Sequence 62 AA;
Query Match 98.3%; Score 169; DB 2; Length 62;
Best Local Similarity 94.3%; Pred. No. 1.2e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDDRADALQXASQFEXSAKLRKRYWMKNLX 35
DB 28 LSELDDRADALQAGASQFESSAAKLRKRYWMKNLX 62
RESULT 7
ADE57598
ID ADE57598 standard; protein; 115 AA.
AC ADE57598;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P19065, SEQ ID NO 3460.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SN1; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-26812/26.
XX
XX GENBANK; P19065.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;
Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDDRADALQXASQFEXSAKLRKRYWMKNLX 35
DB 59 LSELDDRADALQAGASQFETSAAKLRKRYWMKNLX 93
RESULT 8
ADE57612
ID ADE57612 standard; protein; 115 AA.
AC ADE57612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein Q64357, SEQ ID NO 3474.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SN1; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.
DR GENBANK; Q64357.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1, Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQPEXSAAKLKRRYWNKLNK 35
Db 59 LSELDPRADALQAGASQFETSAAKLKRRYWNKLNK 93

RESULT 9
ADE60831
ID ADE60831 standard; protein; 115 AA.

XX ADE60831;

XX 29-JAN-2004 (first entry)

XX Human Protein P19065, SEQ ID NO 6743.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.

XX GENBANK; P19065.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1, Page; 1017pp; English.

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CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQPEXSAAKLKRRYWNKLNK 35
Db 59 LSELDPRADALQAGASQFETSAAKLKRRYWNKLNK 93

RESULT 10
ADE57606
ID ADE57606 standard; protein; 115 AA.

XX ADE57606;

XX 29-JAN-2004 (first entry)

XX Human Protein P19065, SEQ ID NO 3468.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

an
kai; pain; neuronal tissue; gene therapy; spinal segmental motor injury

KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
OS WO2003016475-A2.
XX
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; Q64357.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 115 AA;
SO
Query Match 98.3%; Score 169; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX
XX Rat Protein Q64357, SEQ ID NO 3466.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
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XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; Q64357.
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XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
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CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
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XX Sequence 115 AA;
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Query Match 98.3%; Score 169; DB 7; Length 115;
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XX 29-JAN-2004 (first entry)

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XX AC ADE57596;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein Q64357, SEQ ID NO 3458.
XX KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; Q64357.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017p; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 115 AA;
XX
XX Query Match 98.3%; Score 169; DB 7; Length 115;
XX Best Local Similarity 94.3%; Pred. No. 2,3e-16;
XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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XX DT 29-JAN-2004 (first entry)
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XX KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX KM spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P19065.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017p; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 115 AA;
XX
XX Query Match 98.3%; Score 169; DB 7; Length 115;
XX Best Local Similarity 94.3%; Pred. No. 2,3e-16;
XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Tue Nov 2 10:45:11 2004

us-10-802-574-3.rag

Page 9

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Search completed: November 1, 2004, 18:04:03
Job time : 92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds
(without alignments)
99.035 Million cell updates/sec

Title: US-10-802-574-3

Perfect score: 172
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	169	98.3	35	2	US-08-760-001-11
3	169	98.3	35	2	US-08-015-960-9
4	169	98.3	35	3	US-09-015-960-11
5	169	98.3	35	3	US-09-534-572-9
6	169	98.3	35	3	US-09-534-572-11
7	169	98.3	40	4	US-09-570-022-16
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11	169	98.3	62	2	US-09-015-960-8
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14	169	98.3	116	1	US-08-409-373B-4
15	169	98.3	116	1	US-08-393-985-16
16	169	98.3	116	3	US-08-621-018B-10
17	169	98.3	116	3	US-08-819-286-2
18	169	98.3	116	4	US-09-483-665-10
19	169	98.3	35	4	US-09-962-3608-3
20	169	97.7	82	4	US-08-621-018B-11
21	167	97.1	82	4	US-09-483-665-11
22	164	95.3	100	4	US-08-621-018B-6
23	164	95.3	100	4	US-09-483-665-6
24	164	95.3	103	1	US-08-409-373B-3
25	164	95.3	103	1	US-08-409-373B-3
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27	164	95.3	103	4	US-09-483-665-9

28	164	95.3	347	4	US-09-513-783A-28	Sequence 28, Appl
29	164	95.3	347	4	US-09-430-656-10	Sequence 30, Appl
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ALIGNMENTS

RESULT 1
US-08-760-001-9
Sequence 9, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/CB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32, 893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2643
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-9
Query Match 98.3%; Score 169; DB 2; Length 35;
Best Local Similarity 94.3%; Pred. No. 66-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
US-08-760-001-11
Sequence 11, Application US/08760001

Patent No. 5962637

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,001

FILING DATE: Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/01279

FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32, 893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-760-001-11

Query Match

Best Local Similarity 98.3%; Score 169; DB 2; Length 35;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 LSELDDRADALQAGASQFESSAKLKRYKWNKX 35

US-09-015-960-9
Sequence 9, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32, 893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-015-960-9

Query Match

Best Local Similarity 98.3%; Score 169; DB 3; Length 35;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 LSELDDRADALQAGASQFESSAKLKRYKWNKX 35

US-09-015-960-11
Sequence 11, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-11

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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US-09-534-572-9
Sequence 9, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-534-572-9

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFESXSAKLKRYKWKXK 35
Db 1 LSELDDRADALQAGASQFESXSAKLKRYKWKXK 35

RESULT 6

US-09-534-572-11
Sequence 11, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-11

Query Match 98.3%; Score 169; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 6e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFESXSAKLKRYKWKXK 35
Db 1 LSELDDRADALQAGASQFETSAAKLKRYKWKXK 35

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RESULT 7
US-09-570-022-16
; Sequence 16, Application US/09570022
; Patent No. 6573244
; GENERAL INFORMATION:
; APPLICANT: GORDON, RICHARD K.
; APPLICANT: MOORAD, DEBORAH R.
; APPLICANT: DOCTOR, BHUPENDRA P.
; APPLICANT: GARCIA, GREGORY E.
; TITLE OF INVENTION: PREVENTING AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
; FILE REFERENCE: 38644-170531
; CURRENT APPLICATION NUMBER: US/09/570,022
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,446
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-570-022-16

Query Match          98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7e-18; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40

RESULT 8
US-09-570-023-8
; Sequence 8, Application US/09570023
; Patent No. 6713444
; GENERAL INFORMATION:
; APPLICANT: GARCIA, GREGORY E.
; APPLICANT: MOORAD, RICHARD K.
; APPLICANT: DOCTOR, DEBBIE R.
; APPLICANT: MOORAD, BHUPENDRA P.
; TITLE OF INVENTION: BUFFERIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
; FILE REFERENCE: 37833-20004.00
; CURRENT APPLICATION NUMBER: US/09/570,023
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-570-023-8

Query Match          98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7e-18; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40

RESULT 9
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, JAMES J.
; APPLICANT: STAFFORD, ROBERT G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
US-09-962-360B-9

Query Match          98.3%; Score 169; DB 4; Length 42;
Best Local Similarity 94.3%; Pred. No. 7.4e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    4 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 38

RESULT 10
US-08-760-001-8
; Sequence 8, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; CLASSIFICATION: 530
; FILING DATE: Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-8

Query Match 98.3%; Score 169; DB 2; Length 62;
Best Local Similarity 94.3%; Pred. No. 1.1e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFESSAAKLKRYKWKNLK 35
DB 28 LSELDPRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 11
US-09-015-960-8
Sequence 8, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-8

Query Match 98.3%; Score 169; DB 3; Length 62;
Best Local Similarity 94.3%; Pred. No. 1.1e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFESSAAKLKRYKWKNLK 35
DB 28 LSELDPRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 12
US-09-534-572-8
Sequence 8, Application US/09534572
Patent No. 6337386

GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-8

Query Match 98.3%; Score 169; DB 3; Length 62;
Best Local Similarity 94.3%; Pred. No. 1.1e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFESSAAKLKRYKWKNLK 35
DB 28 LSELDPRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 13
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5585240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Selhamer, Jeffrey J.
TITLE OF INVENTION: CELLUBREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 98.3%; Score 169; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 2,3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

Db 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

RESULT 14
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5650280
Patent No. 5650280 5585240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Sellmeier, Jeffrey J.
TITLE OF INVENTION: CELLULOREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 98.3%; Score 169; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 2,3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

Db 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

RESULT 15
US-08-393-985-16
Sequence 16, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-393-985-16

Query Match 98.3%; Score 169; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 2,3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

Db 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35
60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

Search completed: November 1, 2004, 18:19.41
Job time : 24.4375 secs

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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds
(without alignments)
164.308 Million cell updates/sec

Title: US-10-802-574-3
Sequence: 1 LSELDRADALQXASQFEXSAKLRKYWMXNK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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6: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep:*
8: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubppaa/US09_PUB.pep:*
12: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
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15: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
	1	169	98.3	42	10	US-09-962-360B-9
	2	169	98.3	116	10	US-09-942-024-4
	3	169	98.3	116	10	US-09-942-024-17
	4	169	98.3	116	10	US-09-942-024-18
	5	169	98.3	116	10	US-09-942-024-4
	6	169	98.3	116	10	US-09-942-024-17
	7	169	98.3	116	10	US-09-942-024-18
	8	169	98.3	116	14	US-10-357-028-10
	9	169	98.3	116	15	US-10-261-161-11
	10	169	98.3	116	15	US-10-261-161-12
	11	169	98.3	116	15	US-10-261-161-13
	12	169	98.3	607	10	US-09-293-670-55
	13	168	97.7	35	10	US-09-962-360B-3

14	167	97.1	82	14	US-10-357-028-11	Sequence 11, Appl
15	167	97.1	114	10	US-09-942-024-19	Sequence 19, Appl
16	167	97.1	114	10	US-09-942-024-19	Sequence 19, Appl
17	167	97.1	114	15	US-10-261-161-14	Sequence 14, Appl
18	164	95.3	103	14	US-10-357-028-6	Sequence 6, Appl
19	164	95.3	103	14	US-10-357-028-9	Sequence 9, Appl
20	164	95.3	117	16	US-10-467-595-27	Sequence 27, Appl
21	164	95.3	118	10	US-09-942-024-96	Sequence 96, Appl
22	164	95.3	118	10	US-09-942-024-96	Sequence 96, Appl
23	164	95.3	118	10	US-10-261-161-10	Sequence 10, Appl
24	164	95.3	347	14	US-10-100-957A-28	Sequence 28, Appl
25	164	95.3	350	14	US-10-100-957A-30	Sequence 30, Appl
26	164	95.3	365	10	US-09-293-670-52	Sequence 52, Appl
27	162	94.2	35	10	US-09-962-360B-4	Sequence 4, Appl
28	152	88.4	109	14	US-10-369-493-6364	Sequence 6364, Ap
29	149	86.6	40	10	US-09-942-024-57	Sequence 57, Appl
30	149	86.6	40	10	US-09-942-024-58	Sequence 58, Appl
31	149	86.6	40	10	US-09-942-024-60	Sequence 60, Appl
32	149	86.6	40	10	US-09-942-024-61	Sequence 61, Appl
33	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl
34	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl
35	149	86.6	40	10	US-09-942-024-58	Sequence 58, Appl
36	149	86.6	40	10	US-09-942-024-60	Sequence 60, Appl
37	149	86.6	40	10	US-09-942-024-61	Sequence 61, Appl
38	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl
39	149	86.6	40	15	US-10-261-161-82	Sequence 82, Appl
40	149	86.6	40	15	US-10-261-161-83	Sequence 83, Appl
41	149	86.6	40	15	US-10-261-161-85	Sequence 85, Appl
42	149	86.6	40	15	US-10-261-161-86	Sequence 86, Appl
43	149	86.6	40	15	US-10-261-161-90	Sequence 90, Appl
44	145	84.3	104	10	US-09-942-024-20	Sequence 20, Appl
45	145	84.3	104	10	US-09-942-024-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US2003007685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoreceinyl-glycine
US-09-962-360B-9
Query Match 98.3%; Score 169; DB 10; Length 42;
Best Local Similarity 94.3%; Pred. No. 6,6e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 LSELDRADALQXASQFEXSAKLRKYWMXNK 35
DB 4 LSELDRADALQXASQFEXSAKLRKYWMXNK 38

```
RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQXASQFETSAKLRKRYWKNLK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQXASQFETSAKLRKRYWKNLK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
```

```
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Bos taurus
US-09-942-024-18

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQXASQFETSAKLRKRYWKNLK 94

RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridia1
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-942-098-4

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQXASQFETSAKLRKRYWKNLK 94

RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridia1
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-942-098-17

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Tue Nov 2 10:45:11 2004

us-10-802-574-3.rapb

Page 3

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 7
US-09-942-098-18
Sequence 18, Application US/09942098
Publication No. US20030143651A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Clostridial
FILE REFERENCE: P-AR 4802
CURRENT APPLICATION NUMBER: US/09/942,098
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 116
TYPE: PRT
ORGANISM: Bos taurus
US-09-942-098-18

Query Match 98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 8
US-10-357-028-10
Sequence 10, Application US/10357028
Publication No. US20030180931A1
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Selthamer, Jeffrey J.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/357,028
FILING DATE: 29-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/483,665
FILING DATE: Herewith
APPLICATION NUMBER: 08/621,018
FILING DATE: March 22, 1996
APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-849-8886
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 433075
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

Query Match 98.3%; Score 169; DB 14; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 9
US-10-261-161-11
Sequence 11, Application US/10261161
Publication No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
US-10-261-161-11

Query Match 98.3%; Score 169; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 10
US-10-261-161-12
Sequence 12, Application US/10261161
Publication No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 116
TYPE: PRT

ORGANISM: Mus musculus
US-10-261-161-12

Query Match 98.3%; Score 169; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQEFXSAAKLRRKYWMNLK 35
60 LSELDDRADALQAGASQEFETSAAKLRRKYWMNLK 94

RESULT 11

US-10-261-161-13
Sequence 13, Application US/10261161
Publication No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
APPLICANT: Aoki, Kei-Roger
TITLE OF INVENTION: Cell-based fluorescence resonance energy transfer (FRET) Assays for Clostridial Toxins
FILE REFERENCE: P-AR 4804
CURRENT APPLICATION NUMBER: US/10/261,161
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 116
TYPE: PRF
ORGANISM: Bos taurus
US-10-261-161-13

Query Match 98.3%; Score 169; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQEFXSAAKLRRKYWMNLK 35
60 LSELDDRADALQAGASQEFETSAAKLRRKYWMNLK 94

RESULT 12

US-09-293-670-55
Sequence 55, Application US/09293670
Publication No. US20030190684A1
GENERAL INFORMATION:
APPLICANT: Fisher, Joseph
APPLICANT: Lorens, James
APPLICANT: Payan, Donald
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
FILE REFERENCE: A68104/DJB/RMS/DAV
CURRENT APPLICATION NUMBER: US/09/293,670
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
LENGTH: 607
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-293-670-55

Query Match 98.3%; Score 169; DB 10; Length 607;
Best Local Similarity 94.3%; Pred. No. 9.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQEFXSAAKLRRKYWMNLK 35
60 LSELDDRADALQAGASQEFETSAAKLRRKYWMNLK 94

Db 61 LSELDDRADALQAGASQEFETSAAKLRRKYWMNLK 95

RESULT 13
US-09-962-360B-3
Sequence 3, Application US/09962360B
Publication No. US20030077685A1
GENERAL INFORMATION:
/9
APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 3
LENGTH: 35
TYPE: PRF
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
NAME/KEY: misc feature
LOCATION: 14 and 20
OTHER INFORMATION: Xaa at 14 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 ;
OTHER INFORMATION: (fluoresceiny1)-cysteine
US-09-962-360B-3

Query Match 97.7%; Score 168; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.6e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQEFXSAAKLRRKYWMNLK 35
60 LSELDDRADALQAGASQEFETSAAKLRRKYWMNLK 94

RESULT 14

US-10-357-028-11
Sequence 11, Application US/10357028
Publication No. US20030180931A1
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Sellhammer, Jeffrey J.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: CELLULREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/357,028
FILING DATE: 29-Jan-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/483,665
FILING DATE: Herewith
APPLICATION NUMBER: 08/622,018
FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-843-8886
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 606978
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 97.1%; Score 167; DB 14; Length 82;
Best Local Similarity 91.4%; Pred. No. 2,4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAAASQEFEXSAKLRKRYWKNLK 35
Db 26 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 60

RESULT 15
US-09-942-024-19
Sequence 19, Application US/09942024
Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 114
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-942-024-19

Query Match 97.1%; Score 167; DB 10; Length 114;
Best Local Similarity 91.4%; Pred. No. 3,4e-15;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAAASQEFEXSAKLRKRYWKNLK 35
Db 58 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 92

Search completed: November 1, 2004, 18:23:47
Job time : 70.0625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 18.125 Seconds

(Without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-3

Sequence: 1 LSELDDRADALQAXSQFEXSAKLRKRYWKNLK 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	98.3	116	2 B38315	synaptobrevin 2 -
2	169	98.3	116	2 JN0011	synaptobrevin 2 -
3	169	98.3	116	2 B34288	synaptobrevin 2 -
4	164	95.3	103	2 S35077	celldubrevin - rat
5	164	95.3	118	2 S52747	Vamp1 protein - hu
6	164	95.3	118	2 A38315	synaptobrevin 1 -
7	164	95.3	120	2 A32146	vesicle-associated
8	157	91.3	118	2 A34288	vesicle-associated
9	154	89.5	125	2 S40153	synaptobrevin - lc
10	152	88.4	109	2 T33239	synaptobrevin SNB
11	115	66.9	32	2 S35555	vesicle-associated
12	115	66.9	32	2 S35554	vesicle-associated
13	115	66.9	32	2 S35552	vesicle-associated
14	112	65.1	132	2 J01522	synaptobrevin isof
15	112	65.1	152	2 J01521	synaptobrevin isof
16	108	62.6	32	2 S35553	vesicle-associated
17	106	61.6	145	2 T21338	hypothetical prote
18	87	50.6	223	2 S47654	integral membrane
19	81	47.1	115	2 S62059	synaptobrevin homo
20	75	43.6	121	2 T39073	synaptobrevin homo
21	71	41.3	117	2 S31250	synaptobrevin homo
22	68	39.5	220	2 T00801	probable synaptoch
23	64	37.2	60	2 D44088	homeotic protein H
24	64	37.2	221	2 P84741	probable synaptoch
25	63	36.6	1237	1 GNF42	HIV-1 retropepin
26	62	36.0	175	2 D6180	hypothetical prote
27	59	34.3	251	2 S64927	probable membrane
28	58	33.7	210	2 T16595	hypothetical prote
29	57.5	33.4	229	2 P86180	hypothetical prote

30	57	33.1	240	2 T47589	synaptobrevin-like
31	55	32.0	219	2 T04630	synaptobrevin homo
32	54	31.4	102	2 S44781	C0A5.4 protein -
33	54	31.4	102	2 T24909	hypothetical prote
34	54	31.4	302	2 S69725	hypothetical prote
35	53	30.8	499	2 T18791	gamma-aminobutyric
36	53	30.8	855	2 T29775	hypothetical prote
37	52.5	30.5	2326	2 T29140	hypothetical prote
38	52	30.2	183	1 TUBP84	cat1 fiber assemb
39	52	30.2	183	2 S13240	cat1 fiber assemb
40	52	30.2	788	2 T44262	transducer protein
41	52	30.2	789	2 E84236	Htr6 transducer [i
42	52	30.2	1116	2 T42213	m-tomosyn, isoform
43	51.5	29.9	1278	2 T27925	hypothetical prote
44	51	29.7	609	2 A50500	glutamine-fructose
45	51	29.7	1281	2 U05368	dynactin 1 - mouse

ALIGNMENTS

RESULT 1

B38315

synaptobrevin 2 - human

C/Species: Homo sapiens (man)

C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004

C/Accession: B38315

R/Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.

U. Biol. Chem. 265, 17267-17273, 1990

A/Title: Structures and Chromosomal localizations of two human genes encoding synaptobrevin

A/Reference number: A38315; MID:91009161; PMID:1976629

A/Accession: B38315

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-116 <ARC>

A/Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:G338630; PIDN:AAA60604.1; I

C/Genetics: A:Gene: GDB:SVB2; VAMP-2

A/Cross-references: GDB:125293; OMIM:185881

A/Map position: 17pter-17p12

C/Superfamily: synaptobrevin

C/Keywords: membrane trafficking; transmembrane protein

Query Match 98.3%; Score 169; DB 2; Length 116;

Best Local Similarity 94.3%; Pred. No. 3e-16; Mismatches 2; Indels 0; Gaps 0;

Matches 33; Conservative

QY 1 LSELDDRADALQAXSQFEXSAKLRKRYWKNLK 35

DB 60 LSELDDRADALQAGSQFETSAKLRKRYWKNLK 94

RESULT 2

JN0011

synaptobrevin 2 - bovine

N/Alternate names: SNAP receptor

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: JN0011; S36811; S32363

R/Suedhof, T.C.; Baument, M.; Perin, M.S.; Jahn, R.

Neuron 2, 1475-1481, 1989

A/Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.

A/Reference number: A93413; MID:90180466; PMID:2560644

A/Accession: JN0011

A/Molecule type: mRNA

A/Residues: 1-116 <SUB>

A/Cross-references: UNIPROT:P19065; GB:X76199; NID:G433075; PIDN:CA53792.1; PID:G433076

A/Experimental source: brain

R/Horioka, H.P.M.; Saito, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.

FEBS Lett. 330, 236-240, 1993

A/Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn

A/Reference number: S36811; MID:93374072; PMID:8365494

A/Accession: S36811

A:Molecule type: mRNA
 A:Residues: 'X',48-79 <HOR>
 A:Experimental source: brain
 R:Soelner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Germain, S.; Tem
 Nature 362, 318-324, 1993
 A:Title: SNRP receptor implicated in vesicle targeting and fusion.
 A:Reference number: S32360; MUID:93205116; PMID:8455717
 A:Accession: S32363
 A:Molecule type: protein
 A:Residues: 31-47, 'X',49-55, 'X',57-59;67-82 <SOE>
 A:Experimental source: brain
 C:Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.
 C:Superfamily: synaptobrevin
 C:Keywords: acetylated amino end; membrane trafficking; transmembrane protein
 F/2-116/Product: synaptobrevin 2 #status predicted <MAT>
 F/95-114/Domain: transmembrane #status predicted <TM>
 F/2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 60 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 94

RESULT 3
 B34288
 synaptobrevin 2 - rat
 N:Alternate names: vesicle-associated membrane protein 2
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
 C:Accession: B34288; S27125
 R:Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
 J. Biol. Chem. 264, 11061-11064, 1989
 A:Title: Two vesicle-associated membrane protein genes are differentially expressed in d
 A:Reference number: A34288; MUID:89291844; PMID:2472388
 A:Accession: B34288
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-116 <ELF>
 A:Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:9207626; PIDN:AAA42321.1;
 R:Schlavo, G.; Benetati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; Dasgupta, B.R
 Nature 359, 832-835, 1992
 A:Title: Tetanus and Botulinum-B neurotoxins block neurotransmitter release by proteolyt
 A:Reference number: S27125; MUID:93063293; PMID:1331807
 A:Accession: S27125
 A:Molecule type: protein
 A:Residues: 77-99, 'X',101 <SCH>
 A:Superfamily: synaptobrevin
 C:Keywords: membrane protein; membrane trafficking; synaptic vesicle

Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 60 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 94

RESULT 4
 S35077
 cellubrevin - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S35077
 R:McMahon, H.T.; Uschakov, Y.A.; Edelman, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R
 Nature 364, 346-349, 1993
 A:Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy
 A:Reference number: S35077; MUID:93323976; PMID:8332193
 A:Accession: S35077

A:Molecule type: mRNA
 A:Residues: 1103 <MCW>
 A:Cross-references: UNIPROT:Q64271; GB:S63830; NID:9388482; PIDN:AAE27554.1; PID:9388483
 C:Superfamily: synaptobrevin

Query Match 95.3%; Score 164; DB 2; Length 103;
 Best Local Similarity 91.4%; Pred. No. 1.3e-15;
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 47 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 81

RESULT 5
 S52747
 Vamp1 protein - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S52747
 R:Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frenkel, M.J.; Ward, C.W.
 submitted to the EMBL Data Library, December 1994
 A:Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.
 A:Reference number: S52747
 A:Accession: S52747
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-118 <GOU>
 A:Cross-references: UNIPROT:P23763; EMBL:248924; NID:9758107; PIDN:CAA8760.1; PID:975810
 C:Superfamily: synaptobrevin

Query Match 95.3%; Score 164; DB 2; Length 118;
 Best Local Similarity 91.4%; Pred. No. 1.5e-15;
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 62 LSELDPRADALQXASQFESSAAKLRKRYWKNLK 96

RESULT 6
 A38315
 synaptobrevin 1 - human
 C:Species: Homo sapiens (man)
 C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A38315
 R:Archer III, B.T.; Oezcelik, T.; Jahn, R.; Franke, U.; Suedhof, T.C.
 J. Biol. Chem. 265, 17267-17273, 1990
 A:Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
 A:Reference number: A38315; MUID:91009161; PMID:1976629
 A:Accession: A38315
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <ARC>
 A:Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:9338623; PIDN:AAA60503.1; I
 C:Genetics:
 A:Gene: GDB:SYB1; VAMP-1
 A:Cross-references: GDB:125292; OMIM:185880
 A:Map position: 12p-12p
 C:Superfamily: synaptobrevin
 C:Keywords: membrane trafficking; transmembrane protein

Query Match 95.3%; Score 164; DB 2; Length 118;
 Best Local Similarity 91.4%; Pred. No. 1.5e-15;
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35
 |||||
 62 LSELDPRADALQXASQFESSAAKLRKRYWKNLK 96

RESULT 7
 A32146


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OX NCB1_TaxID=8364;
RN 11)
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC061396; AAH61396.1; -
DR InterPro; IPR001388; Synaptoleucin.
DR Pfam; PF00957; Synaptoleucin; 1.
DR PRINTS; PR00219; SYNAPTOLEUCIN.
DR PRODOM; PD001229; Synaptoleucin; 1.
DR PROSITE; PS00417; SYNAPTOLEUCIN; 1.
DR PROSITE; PS00892; V_SNAKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDFF2A1ABE CRC64;

Query Match 98.3%; Score 169; DB 2; Length 114;
Best Local Similarity 94.3%; Pred. No. 7.2e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAXASQFEXSAKLRKXYWKNLK 35
DB 58 LSELDDRADALQAGASQFETSAAKLRKXYWKNLK 92

RESULT 3
AAH61396 PRELIMINARY; PRT; 114 AA.
AC AAH61396;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGCT5977.
GN MGCT5977.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCB1_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

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RA Brownstein M.J., Uedlin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC061396; AAH61396.1; -
DR InterPro; IPR001388; Synaptoleucin.
DR Pfam; PF00957; Synaptoleucin; 1.
DR PRINTS; PR00219; SYNAPTOLEUCIN.
DR PRODOM; PD001229; Synaptoleucin; 1.
DR PROSITE; PS00417; SYNAPTOLEUCIN; 1.
DR PROSITE; PS00892; V_SNAKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDFF2A1ABE CRC64;

Query Match 98.3%; Score 169; DB 2; Length 114;
Best Local Similarity 94.3%; Pred. No. 7.2e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAXASQFEXSAKLRKXYWKNLK 35
DB 58 LSELDDRADALQAGASQFETSAAKLRKXYWKNLK 92

RESULT 4
VAMP2 HUMAN STANDARD; PRT; 115 AA.
AC P19065;
DT 01-NOV-1990 (Ref. 16, Created)
DT 01-NOV-1997 (Ref. 35, Last sequence update)
DT 01-OCT-2004 (Ref. 45, Last annotation update)
DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptoleucin 2).
GN Name=VAMP2; Synonyms=SYB2;
OS Homo sapiens (Human); and
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCB1_TaxID=9606; 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=91009161; PubMed=1976629;
RA Archer B.T. III, Oezcelik T., Jahn R., Francke U., Suedhof T.C.;
RT "Structures and chromosomal localizations of two human genes encoding
RT synaptoleucins 1 and 2."
RL J. Biol. Chem. 265:117267-117273(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Peripheral blood;
RA Nabokina S.M., Iazo P.A., Mollienedo F.;
RT "Expression of VAMP genes in human neutrophils."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Blood;
RA Tarnusio D., Zorag K.G., Falbo V.;
RT "Genomic structure of human SYB2 gene."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=90180466; PubMed=2560644;
RA Suedhof T.C., Baumert M., Perin M.S., Jahn R.;
RT "A synaptic vesicle membrane protein is conserved from mammals to
RT Drosophila."

```

RL Neuron 2:1475-1481(1989).

RN [5]

RC SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.

RP SPECIES=Bovine.

RX MEDLINE=93205116; PubMed=8455717;

RA Soeller T., Whiteheart S.W., Brunner M., Erdjument-Bromage H., Geramios S., Tempst P., Rothman J.E.;

RT "SNAP receptors implicated in vesicle targeting and fusion.";

RL Nature 362:318-324(1993).

RN [6]

RP TISSUE SPECIFICITY.

RC SPECIES=Human.

RX MEDLINE=9633494; PubMed=8760387;

RA Jagadeesh M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J., Ward C.W.;

RT "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";

RL Biochem. J. 317:945-954(1996).

RN [7]

RP TOPOLOGY.

RC SPECIES=Human.

RX MEDLINE=95137000; PubMed=7835332;

RA Kuray U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;

RT "Transport route for synaptobrevin via a novel pathway of insertion into the endoplasmic reticulum membrane.";

RL EMBO J. 14:217-223(1995).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-68 IN COMPLEX WITH BOTB.

RC SPECIES=Human.

RX MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;

RA Hanson M.A., Stevens R.C.;

RT "Cocystal structure of synaptobrevin-II bound to botulinum neurotoxin type B at 2.0 A resolution.";

RL Nat. Struct. Biol. 7:687-692(2000).

CC -1- FUNCTION: Involved in the targeting and/or fusion of transport vesicles to their target membrane.

CC -1- SUBUNIT: Interacts with VAMP and VAB.

CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic vesicles.

CC -1- TISSUE SPECIFICITY: Nervous system and skeletal muscle.

CC -1- SIMILARITY: Belongs to the synaptobrevin family.

CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.

CC -----

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CC -----

DR EMBL; M36205; AAA60604.1; -; JOINED.

DR EMBL; M36201; AAA60604.1; -; JOINED.

DR EMBL; M36202; AAA60604.1; -; JOINED.

DR EMBL; M36203; AAA60604.1; -; JOINED.

DR EMBL; M36204; AAA60604.1; -; JOINED.

DR EMBL; A7255044; CAA12385.1; -; -;

DR EMBL; AF155372; AA115551.1; -; -;

DR EMBL; X76199; CAA53792.1; -; -;

DR PIR; B38315; B38315.

DR PIR; JN0011; JN0011.

DR PDB; 1F83; X-ray; B=52-75, C=76-87.

DR Gene; HGNC:12643; VAMP2.

DR MIM; 185881; -;

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR InterPro; IPR001388; Synaptobrevin.

DR Pfam; PF00957; Synaptobrevin_1.

DR PRINTS; PR00219; SYNAPTOBREVN.

DR ProDom; PD001229; Synaptobrevin_1.

DR PROSITE; PS00417; SYNAPTOBREVN; 1.

DR PROSITE; PS50892; V_SNARE; 1.

KW 3D-structure, Acetylation, Coiled coil, Direct protein sequencing;

FT INIT MET 0 0

FT DOMAIN 1 93 Cytoplasmic (potential).

FT TRANSMEM 94 113 Anchor for type IV membrane protein (potential).

FT DOMAIN 114 115 Vesicular (potential).

FT MOD_RES 1 1 N-acetylserine.

FT DOMAIN 30 90 v-SNARE coiled-coil homology.

SQ SEQUENCE 115 AA; 12517 MW; 388B79F0D21AD81E CSeq64;

Query Match 98.3%; Score 169; DB 1; Length 115;

Best Local Similarity 94.3%; Pred. No. 7,3e-16;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISELDPRDALQAXASQFEXSAKIKRYWKTK 35

Db 59 ISELDPRDALQAGASQFETSMAKIKRYWKTK 93

RESULT 5

ID VAMP2_MOUSE STANDARD; PRT; 115 AA.

AC 064357;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).

GN Name=Vamp2; Synonyms=Synd2;

OS Mus musculus (Mouse); and

OS Rattus norvegicus (Rat);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090, 10116;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=Rat;

RX MEDLINE=89291844; PubMed=2472368;

RA Eiferink L.A., Trimble W.S., Scheller R.H.;

RT "Two vesicle-associated membrane protein genes are differentially expressed in the rat central nervous system.";

RL J. Biol. Chem. 264:11061-11064(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=Mouse;

RX MEDLINE=98104125; PubMed=9430681;

RA Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;

RT "Vesicle-associated membrane protein 2 plays a specific role in the insulin-dependent trafficking of the facilitative glucose transporter GLUT4 in 3T3-L1 adipocytes.";

RL J. Biol. Chem. 273:1444-1452(1998).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A AND SNAP25.

RC SPECIES=Rat;

RX MEDLINE=8430524; PubMed=9759724; DOI=10.1038/26412;

RA Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;

RT "Crystal structure of a SNARE complex involved in synaptic exocytosis at 2.4 A resolution.";

RL Nature 395:347-353(1998).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A; CPEX1 AND SNAP25, AND NMR ANALYSIS.

RC SPECIES=Rat;

RX MEDLINE=21822661; PubMed=11832227;

RA Chen X., Tomchick D.R., Kovrig E., Arac D., Machius M., Suedhof T.C., Rizo J.;

RT "Three-dimensional structure of the complexin/SNARE complex.";

RL Neuron 33:397-409(2002).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A AND SNAP25.

RC SPECIES=Rat;

```

RX MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211869200;
RA Ernst U.A., Brunker A.T.;
RT "High resolution structure, stability, and synaptobrevin binding of a
RL truncated neuronal SNARE complex.";
RJ J. Biol. Chem. 278:8630-8636 (2003).
CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
CC vesicles to their target membrane.
CC -1- SUBUNIT: Interacts with VAMP and VAMP2 (by similarity). Part of the
CC SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC complex binds to CPLX1.
CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC vesicles.
CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC expression is seen in the brain as compared to the spinal cord.
CC -1- SIMILARITY: Belongs to the synaptobrevin family.
CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24105; AAA42321.1; -
CC EMBL; U60150; AAB03463.1; -
CC PIR; B34288; B34288.
CC PDB; 1KTL; X-ray; A=26-91.
CC PDB; 1N7S; X-ray; A=26-88.
CC PDB; 1SFC; X-ray; A/E/I=1-95.
CC MGD; MG1:131277; Vamp2.
CC RGD; 3949; Vamp2.
CC InterPro; IPR001388; Synaptobrevin.
CC Pfam; PF00957; Synaptobrevin; 1.
CC PRINTS; PR00219; SYNAPTOBREVIN.
CC PRODOM; PD001229; Synaptobrevin; 1.
CC PROSITE; PS00417; SYNAPTOBREVIN; 1.
CC 3D-structure; Acetylation; Coiled coil; Multigene family;
CC Polymorphism; Synapse; Synaptosome; Transmembrane.
CC INIT MET 0 By similarity.
CC DOMAIN 1 93 Cytoplasmic (Potential).
CC TRANSMEM 94 113 Anchor for type IV membrane protein
CC FT 114 115 (Potential).
CC FT MOD_RES 1 1 Vesicular (Potential).
CC FT DOMAIN 30 90 N-acetylsuxine (By similarity).
CC FT VARIANT 110 110 V-SNARE coiled-coil homology.
CC FT VARIANT 111 111 I -> II.
CC FT HELIX 111 111 V -> I.
CC FT 128 87
CC SEQUENCE 115 AA; 12559 MW; EA400D6291ABF0BC CRC64;
SQ
Query Match 98.3%; Score 169; DB 1; Length 115;
Best Local Similarity 94.3%; Pred. No. 7.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLX 35
DB 59 LSELDDRADALQXASQFETSAKLRKRYWKNLX 93

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC NCBI_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=Brain, Lung, and Testis;
CC MEDLINE=22388257; PubMed=12477932;
CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC Datsenko L., Marais A.K., Farmer A.A., Rubin G.M., Hong L.,
CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Fange C.,
CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
CC Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hult S.W.,
CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC Raiten J., Helton E., Ketterman W., Madan A., Rodriguez S., Sanchez A.,
CC Watling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
CC Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
CC Jones S.J., Marra M.A.;
CC "Generation and initial analysis of more than 15,000 full-length human
CC and mouse cDNA sequences";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC [2]
CC SEQUENCE FROM N.A.
CC TISSUE=Brain;
CC Strausberg R.;
CC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE FROM N.A.
CC TISSUE=Testis;
CC Strausberg R.;
CC Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC [4]
CC SEQUENCE FROM N.A.
CC Strausberg R.;
CC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC EMBL; BC002737; AA02737.3; -
CC EMBL; BC019608; AA119608.1; -
CC EMBL; BC033870; AA133870.1; -
CC HSP; O9MWM2; 1SFC.
CC InterPro; IPR001388; Synaptobrevin.
CC Pfam; PF00957; Synaptobrevin; 1.
CC PRINTS; PR00219; SYNAPTOBREVIN.
CC PRODOM; PD001229; Synaptobrevin; 1.
CC PROSITE; PS00417; SYNAPTOBREVIN; 1.
CC DR PROSITE; PS00892; V-SNARE; 1.
CC SEQUENCE 116 AA; 12663 MW; 9CD679C4FF1B5A8 CRC64;
SQ
Query Match 98.3%; Score 169; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDDRADALQXASQFETSAKLRKRYWKNLX 35
DB 60 LSELDDRADALQXASQFETSAKLRKRYWKNLX 94

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RESULT 6
Q9BUC2 PRELIMINARY; PRT; 116 AA.
AC Q9BUC2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN Name=VAMP2;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 7
Q9NOYO PRELIMINARY; PRT; 116 AA.
AC Q9NOYO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VAMP-2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

```

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hipocampus;
 RA Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: At240769; AAF64476.1; -
 DR HSSP: Q9MUW2; ISFC.
 DR InterPro: IPR01388; Synaptobrevin.
 DR Pfam: PF00557; Synaptobrevin.1.
 DR PRINTS: PR00219; SYNAPTOBREVN.
 DR ProDom: PD001229; Synaptobrevin.1.
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE: PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12653 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLKRYKWKXNLK 35
 DB 60 LSELDPRADALQAGASOFETSAAKLKRYKWKXNLK 94

RESULT 8
 O35619 PRELIMINARY; PRT; 116 AA.
 ID O35619;
 AC O35619;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Vesicle associated membrane protein 2.
 GN Name=Vamp2; Synonyms=mvAMP-2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsen S.K., Doeire S., Corley R.B.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF007168; AAB62931.1; -
 DR PIR: S35554; S35554.
 DR HSSP: Q9MUW2; ISFC.
 DR MGD: MGI:1313277; Vamp2.
 DR GO: GO:0030141; C:secretory granule; IDA.
 DR GO: GO:0030672; C:synaptic vesicle membrane; IDA.
 DR GO: GO:0042589; C:zymogen granule membrane; IDA.
 DR GO: GO:0005516; F:calmodulin binding; IDA.
 DR GO: GO:0005543; F:phospholipid binding; IDA.
 DR GO: GO:0000149; F:SNARE binding; IDA.
 DR GO: GO:0017156; P:calcium ion-dependent exocytosis; IDA.
 DR GO: GO:0017157; P:regulation of exocytosis; IDA.
 DR InterPro: IPR01388; Synaptobrevin.
 DR Pfam: PF00957; Synaptobrevin.1.
 DR PRINTS: PR00219; SYNAPTOBREVN.
 DR ProDom: PD001229; Synaptobrevin.1.
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE: PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4R1DD565549D0A CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLKRYKWKXNLK 35
 DB 60 LSELDPRADALQAGASOFETSAAKLKRYKWKXNLK 94

RESULT 9
 AAH02737 PRELIMINARY; PRT; 116 AA.
 ID AAH02737;
 AC AAH02737;
 DT 14-APR-2004 (TREMBLrel. 27, Created)
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).
 GN VAMP2
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marstina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Utsal T.B., Toshiki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalske U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002737; AAH02737.3; -
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLKRYKWKXNLK 35
 DB 60 LSELDPRADALQAGASOFETSAAKLKRYKWKXNLK 94

RESULT 10
 AAH55105 PRELIMINARY; PRT; 116 AA.
 ID AAH55105;
 AC AAH55105;
 DT 14-APR-2004 (TREMBLrel. 27, Created)
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DE Vesicle-associated membrane protein 2.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Buterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.,
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC055105; AAH55105.1; -
 DR SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;
 SQ
 Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSELDRADALQAXAQEFXSAAKLKRYKWWXNLK 35
 Db 60 LSELDRADALQAGSQFETSAKLKRYKWWXNLK 94
 RESULT 11
 BAC41125 PRELIMINARY; PRT; 116 AA.
 AC BAC41125;
 DT 14-APR-2004 (TREMBLrel. 27, Created)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DE 15 days embryo brain cDNA, RIKEN full-length enriched library,
 DE clone:G630012G02 product:unclassified, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573(2002).
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690(2001).
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RA "High-efficiency full-length cDNA cloning.";
 Meth. Enzymol. 303:19-44(1999).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 Genome Res. 10:1617-1630(2000).
 RL [5]
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771(2000).
 RL [6]
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Adachi J., Aizawa K., Akimura T., Arahawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nomazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK090178; BAC41125.1; -
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;
 Query Match 98.3%; Score 169; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSELDRADALQAXAQEFXSAAKLKRYKWWXNLK 35
 Db 60 LSELDRADALQAGSQFETSAKLKRYKWWXNLK 94
 RESULT 12
 O9QWU2 PRELIMINARY; PRT; 135 AA.
 AC O9QWU2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Vesicle associated membrane protein 2B.
 GN Name=vamp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99257576; PubMed=10371166;
 RA Mandic R., Lowe A.W.,
 RT "Characterization of an alternatively spliced isoform of rat vesicle
 RT associated membrane protein-2 (VAMP-2)."
 FEBS Lett. 451:209-213(1999).
 RL EMBL: AJ133104; CAB43509.1; -
 DR Interpro: IPR001388; SynaptoBrevin.
 DR Pfam: PF00357; SynaptoBrevin.1.
 DR PRINTS: PR00219; SYNAPTOBREVN.
 DR ProDom: PD001229; SynaptoBrevin.1.

Search completed: November 1, 2004, 17:59:09
 Job time : 99.1875 secs

Query Match 97.1%; Score 167; DB 1; Length 113;
 Best Local Similarity 91.4%; Pred. No. 1.4e-15;
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFETSAKLRKXYWKNLK 35
 DB 57 LSELDPRADALQAXASQFETSAKLRKXYWKNMK 91

RESULT 15

AAH60344 PRELIMINARY; PRT; 114 AA.

AAH60344; AAH60344;

02-MAR-2004 (TREMBlrel. 27, Created)

02-MAR-2004 (TREMBlrel. 27, Last sequence update)

02-MAR-2004 (TREMBlrel. 27, Last annotation update)

Vamp2-B-piov protein.

VAMP2-B-PROV.

Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

NCBI_TaxID=8355;

SEQUENCE FROM N.A.

TISSUE=Embryo;

MEDLINE=22341132; PubMed=12454917;

Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

Richardson P.;

"Genetic and genomic tools for Xenopus research: The NIH Xenopus

initiative.";

Dev. Dyn. 225:384-391 (2002).

SEQUENCE FROM N.A.

TISSUE=Embryo;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein W.J., Ustin T.B., Toshbiky S., Cantinci P., Plange C.,

Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,

Jones S.J., Mair M.A.;

"Generation and initial analysis of more than 15,000 full-length human

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

SEQUENCE FROM N.A.

TISSUE=Embryo;

Klein S., Strausberg R.;

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

EMBL; BC060344; AAH60344.1; -

SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2D1DBF CRC64;

Query Match 97.1%; Score 167; DB 2; Length 114;

Best Local Similarity 91.4%; Pred. No. 1.4e-15;

Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFETSAKLRKXYWKNLK 35

DB 58 LSELDPRADALQAXASQFETSAKLRKXYWKNMK 92

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 / Search time 90 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-4

Perfect score: 173
Sequence: 1 LSELDDRADALQAGSXFEKSAKUKRKYWNKX 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_238904:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	37	2	AAR86822 VAMP isof
2	170	98.3	40	4	AAB50301 VAMP2 pep
3	170	98.3	40	4	AAB48582 VAMP2 pep
4	170	98.3	42	5	AA015163 Clostridi
5	170	98.3	54	3	AAB39482 Gene 49 h
6	170	98.3	62	2	AAR86821 VAMP isof
7	170	98.3	115	7	ADE57598 Human Pro
8	170	98.3	115	7	ADE57612 Rat Prote
9	170	98.3	115	7	ADE60831 Human Pro
10	170	98.3	115	7	ADE57606 Human Pro
11	170	98.3	115	7	ADE60829 Rat Prote
12	170	98.3	115	7	ADE57600 Rat Prote
13	170	98.3	115	7	ADE57604 Rat Prote
14	170	98.3	115	7	ADE57596 Rat Prote
15	170	98.3	115	7	ADE57602 Human Pro
16	170	98.3	115	7	ADE57610 Human Pro
17	170	98.3	115	7	ADE57592 Rat Prote
18	170	98.3	115	7	ADE57594 Human Pro
19	170	98.3	115	7	ADE57614 Human Pro
20	170	98.3	115	7	ADE57608 Rat Prote
21	170	98.3	116	2	AAW30104 Vesicle-a
22	170	98.3	116	2	AAW43425 Rat Vesic
23	170	98.3	116	3	AAV88243 Bovine sy
24	170	98.3	116	5	ABP43681 VAMP-2 se
25	170	98.3	116	6	ABP76220 Human GEN

26	170	98.3	116	6	AAE36664 Human VAM
27	170	98.3	116	7	ABW01719 Bovine VA
28	170	98.3	116	7	ABW01718 Mouse VAM
29	170	98.3	116	7	ABW01705 Human VAM
30	170	98.3	116	7	ADG89011 Bovine sy
31	170	98.3	116	8	ADM97006 Mouse VAM
32	170	98.3	116	8	ADM97007 Bovine VA
33	170	98.3	116	8	ADM97005 Human VAM
34	170	98.3	368	3	AAV43843 Amino aci
35	170	98.3	368	3	ADF90403 Rat VAMP-
36	170	98.3	608	3	AAV43845 Amino aci
37	170	98.3	609	3	ADF90406 Rat VAMP-
38	169	97.7	35	5	AAO15158 Clostridi
39	168	97.1	82	3	AAV88244 Xenopus s
40	168	97.1	82	7	ADG89012 Frog VAMP
41	168	97.1	114	7	ABW01720 Frog VAMP
42	168	97.1	114	8	ADM97008 Frog VAMP
43	165	95.4	35	2	AAR86824 VAMP isof
44	165	95.4	100	2	AAW04182 Cellubrev
45	165	95.4	100	3	AAV88240 Human cel

ALIGNMENTS

RESULT 1
ID AAR86822 standard; peptide: 37 AA.
AC AAR86822;
XX
DT 15-AUG-1996 (first entry)
XX
DE VAMP isoform-1 residues 60-94 (plus N- and C-terminal cysteines).
XX
XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulinism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= N-terminal Cysteine
FT FT /note= "may be present to attach peptide to solid-phase"
FT Peptide 2..36
FT FT /note= "VAMP isoform-1 residues 60-94"
FT FT Misc-difference 37 /label= C-terminal cysteine
FT FT /note= "may be present to attach to peptide to solid-phase"
XX
XX W09533850-A1.
XX
XX 14-DEC-1995.
XX
XX 02-JUN-1995; 95WO-GB001279.
XX
XX 03-JUN-1994; 94GB-00011138.
XX
XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.
XX (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
XX Shone CC, Hallis B, James BAF, Quinn CP,
XX WPI; 1996-040249/04.
XX
XX Assay for botulinum or tetanus toxin - by combining test cpd. with
XX substrate which is cleaved by the toxin, and antibody specific for the
XX cleaved but not uncleaved substrate.
XX
XX Example 1; Page 28-29; 48pp; English.
XX

/note="The peptide is cleaved between these two residues
by the clostridial neurotoxin"

FT FT /note="The peptide is cleaved between these two residues
XX FT by the clostridial neurotoxin"
XX
PN WO200225284-A2.
XX
XX
XX 28-MAR-2002.
XX
XX 25-SEP-2001; 2001WO-US030188.
XX
XX 25-SEP-2000; 2000US-0235050P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Schmidt JJ, Stafford RG;
XX WPI; 2002-499829/53.
XX
XX Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
XX Claim 24; Page 15; 48pp; English.
XX
XX The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
CC activities of clostridial neurotoxins. The clostridial (including the
CC clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 42 AA;
Query Match 98.3%; Score 170; DB 5; Length 42;
Best Local Similarity 94.3%; Pred. No. 5, 5e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
Db 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38
RESULT 5
AAB39482
ID AAB39482 standard; protein; 54 AA.
XX
XX AAB39482;
XX
XX 02-FEB-2001 (first entry)
XX
XX Gene 49 human secreted protein homologous amino acid sequence #141.
XX
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW noctropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
KW food additive; preservative; chromosome identification; cancer;
KW female reproductive system disorder; immune disorder; wound healing;
KW cardiovascular disorder; neurological disease; infectious disease;
XX infection.
XX
XX Bos taurus.
XX OS
XX WO200058340-A2.
XX PN
XX 05-OCT-2000.
XX
XX 23-MAR-2000; 2000WO-US007724.
XX PF
XX 26-MAR-1999; 99US-0126510P.
XX PR

PR 07-JUN-2000; 2000US-0174850P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis G;
XX WPI; 2000-594638/56.
XX
XX Fifty nucleic acid molecules encoding human secreted proteins, useful in
PT the prevention, treatment and diagnosis of cancer, immune disorders,
PT cardiovascular disorders and neurological diseases.
XX
XX Disclosure; Page 390; 391pp; English.
XX
XX The polynucleotide sequences given in AAC74337 to AAC74386 encode the
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to
CC AAB39484 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
CC vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC cardiant. The polynucleotides and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
CC can also be used as a food additive or preservative to increase or
CC decrease storage capabilities. The polynucleotide are useful for
CC chromosome identification. They are also useful as probes for diagnosing
CC a disorder related to the female reproductive system, particularly breast
CC and/or ovarian cancer. They are also useful in the gene therapy of breast
CC cancer and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,
CC agonists and antagonists are useful in the diagnosis, treatment and
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 54 AA;
Query Match 98.3%; Score 170; DB 3; Length 54;
Best Local Similarity 94.3%; Pred. No. 7, 3e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
Db 20 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 54
RESULT 6
AAB6821
ID AAB6821 standard; peptide; 62 AA.
XX
XX AAB6821;
XX
XX 15-AUG-1996 (first entry)
XX
XX VAMP isoform-1 residues 33-94.
XX
XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
XX Synthetic.
XX OS
XX MO9533850-A1.
XX PN
XX 14-DEC-1995.
XX
XX 02-JUN-1995; 95WO-GB001279.
XX PF
XX 03-JUN-1994; 94GB-00011138.
XX PR

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX

PI Shone CC, Hallis B, James BAF, Quinn CP;
XX WPI, 1996-040249/04.
XX

PT Assay for botulinum or tetanus toxin - by combining test cpd. with
XX substrate which is cleaved by the toxin, and antibody specific for the
XX cleaved but not uncleaved substrate.

PS Example 3; Page 28; 48pp; English.

XX The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the
CC protein VAMP (vesicle-associated membrane protein) at an identical site
CC to that of botulinum toxin type B (BoNT/B). The specificities of the
CC endopeptidase activities of the two toxins however differ in the minimum
CC peptide substrate size required for cleavage. While BoNT/B requires
CC peptide substrates of 30-35 residues in length for optimal cleavage, the
CC requirement for tetanus toxin is peptide substrates of >50 residues in
CC length. The present sequence, VAMP isoform-1 residues 33-94, is a
CC suitable substrate for tetanus toxin

XX Sequence 62 AA;

XX Query Match

Best Local Similarity 98.3%; Score 170; DB 2; Length 62;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 7
XX ADE57598
XX ADE57598 standard; protein; 115 AA.
XX

AC ADE57598;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein P19065, SEQ ID NO 3460.

DE Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX

OS Homo sapiens.
XX
XX WO2003016475-A2.
XX

XX 27-FEB-2003.
XX

XX 14-AUG-2002; 2002WO-US025765.
XX

XX 14-AUG-2001; 2001US-0312147P.
XX

XX 01-NOV-2001; 2001US-0346382P.
XX

XX 26-NOV-2001; 2001US-033347P.
XX

XX (GEHO) GEN HOSPITAL CORP.
XX

XX (FARB) BAYER AG.
XX

XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
XX

XX DR GENBANK; P19065.
XX

PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 115 AA;

QY Query Match
Best Local Similarity 98.3%; Score 170; DB 7; Length 115;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 59 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 93

RESULT 8
XX ADE57612
XX ADE57612 standard; protein; 115 AA.
XX

AC ADE57612;
XX

XX 29-JAN-2004 (first entry)
XX

DE Rat Protein Q64357, SEQ ID NO 3474.
XX

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX

XX Rattus norvegicus.
XX

XX WO2003016475-A2.
XX

XX 27-FEB-2003.
XX

XX 14-AUG-2002; 2002WO-US025765.
XX

XX 14-AUG-2001; 2001US-0312147P.
XX

XX 01-NOV-2001; 2001US-0346382P.
XX

XX 26-NOV-2001; 2001US-033347P.
XX

XX (GEHO) GEN HOSPITAL CORP.
XX

XX (FARB) BAYER AG.
XX

XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
XX

XX DR GENBANK; P19065.
XX

XX WPI; 2003-266312/26.
DR GENBANK; Q64357.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 115 AA;
Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 LSELDDRADALQAGASXFEKSAKLKRYKWKNLK 35
DB 59 LSELDDRADALQAGASQFETSAAKLKRYKWKNLK 93
RESULT 9
ID ADE60831 standard; protein; 115 AA.
AC ADE60831;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein P19065, SEQ ID NO 6743.
DE
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
PR

XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-266312/26.
DR GENBANK; P19065.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 115 AA;
Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 LSELDDRADALQAGASXFEKSAKLKRYKWKNLK 35
DB 59 LSELDDRADALQAGASQFETSAAKLKRYKWKNLK 93
RESULT 10
ID ADE57606 standard; protein; 115 AA.
AC ADE57606;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein P19065, SEQ ID NO 3468.
DE
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
PD

PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; P19065.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKTKRKTYWKNLK 35
Db 59 LSELDDRADALQAGASQFETSAKTKRKTYWKNLK 93

RESULT 11

ADBE0829 ADE60829 standard; protein; 115 AA.

XX ADE60829;

DT 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 6741.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX

PN W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; Q64357.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 170; DB 7; Length 115;
Best Local Similarity 94.3%; Pred. No. 1.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKTKRKTYWKNLK 35
Db 59 LSELDDRADALQAGASQFETSAKTKRKTYWKNLK 93

RESULT 12

ADBE57600 ADE57600 standard; protein; 115 AA.

XX ADE57600;

DT 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 3462.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX
PF 14-AUG-2002. 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; Q64357.
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a rat protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 115 AA;

Query Match	98.3%;	Score 170;	DB 7;	Length 115;
Best Local Similarity	94.3%;	Pred. No. 1.7e-17;		
Matches 33;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

QY 1 LSELDDRADALQAGASXFEFSAAKIKRKYWMNLK 35
| | | | | | | | | | | | | | | | | | | |
Db 59 LSELDDRADALQAGASQFEFSAAKIKRKYWMNLK 93

RESULT 13
ADES7604
ID ADES7604 standard; protein; 115 AA.
XX
XX ADES7604;
DT 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 3466.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX
XX W02003016475-A2.
PN
XX 27-FEB-2003.
PD
XX
PF 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
PI Woolf C, D'Urso D, Befort K, Costigan M,
PS
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 115 AA:

	Query Match	98.3%	Score 170,	DB 7,	Length 115;
	Best Local Similarity	94.3%;	Pred. No. 1,7e-17;		
	Matches 33;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0.

1 LSELDPRADALQAGASXPEXSAAKLKKRYWKNLX 35
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59 LSELDPRADALQAGASCFETSAALKRKYWKNLK 93
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RESULT 14
ADE57596
ID ADE57596 standard; protein; 115 AA.

XX		ADBS7596;				
AC						
DT		29-JAN-2004	(first entry)			
XX						
DB		Rat Protein Q64357,	SEQ ID NO 3458.			
KM		Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;				
XX		chronic constriction injury; CCI; spared nerve injury; SNI; Chung.				
OS		Rattus norvegicus.				
PN		MO2003016475-A2.				
FD		27-FEB-2003.				
XX						
PF		14-AUG-2002;	200ZMO-US025765.			
PR		14-AUG-2001;	200IUS-0312147P.			
PR		01-NOV-2001;	200IUS-0346382P.			
XX		26-NOV-2001;	200IUS-0333347P.			
PA		(GENO) GEN HOSPITAL CORP.				
XX		(FARB) BAYER AG.				
PJ		WOOLF C, D'URSO D, Befort K, Costigan M;				
DR		WPI; 2003-268312/26.				
XX		GEMBANK; Q64357.				
PP		New composition comprising two or more isolated polypeptides, useful for				
PT		preparing a medicament for treating pain in an animal.				
PS		Claim 1; Page; 1017pp; English.				
CC		The invention discloses a composition comprising two or more isolated rat				
CC		or human polynucleotides or a polynucleotide which represents a fragment,				
CC		derivative or allelic variation of the nucleic acid sequence. Also				
CC		claimed are a vector comprising the novel polynucleotide, a host cell				
CC		comprising the vector, a method for identifying a nucleotide sequence				
CC		which is differentially regulated in an animal subjected to pain and a				
CC		kil to perform the method, an array, a method for identifying an agent				
CC		that increases or decreases the expression of the polynucleotide sequence				
CC		that is differentially expressed in neuronal tissue of a first animal				
CC		subjected to pain, a method for identifying a compound which regulates				
CC		the expression of a polynucleotide sequence which is differentially				
CC		expressed in an animal subjected to pain, a method for identifying a				
CC		compound that regulates the activity of one or more of the				
CC		polynucleotides, a method for producing a pharmaceutical composition, a				
CC		method for identifying a compound or small molecule that regulates the				
CC		activity in an animal of one or more of the polypeptides given in the				
CC		specification, a method for identifying a compound useful in treating				
CC		pain and a pharmaceutical composition comprising the one or more				
CC		polypeptides or their antibodies. The polynucleotide or the compound that				
CC		modulates its activity is useful for preparing a medicament for treating				
CC		pain (e.g. spinal segmental nerve injury (SNI), chronic constriction				
CC		injury (CCI) and spared nerve injury (SNR)) in an animal (e.g. gene				
CC		therapy). The sequence presented is a rat protein (shown in Table 2 of				
CC		the specification) which is differentially expressed during pain. Note:				
CC		The sequence data for this patent did not form part of the printed				
CC		specification, but was obtained in electronic form directly from WIPO at				
XX		ftp.wipo.int/pub/published_pct_sequences.				
XX						
SQ		Sequence 115 AA:				
Query Match	96.3%;	Score 170;	DB 7;	Length 115;		
Best Local Similarity	94.3%;	Fred. No. 1.7e-17;				
Matches 33;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0		

RESULT 15
 AD557602 ID AD557602 standard; protein: 115 AA.
 AC AD557602;
 DT 29-JAN-2004 (first entry)
 XX Human Protein P19065, SEQ ID NO 3464.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS
 PN MO2003016475-A2.
 PD 27-FEB-2003.
 PP 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-033347P.
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'Urso D, Befort K, Costigan M;
 DR WPI; 2003-266312/26.
 DR GENBANK; P19065.
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page: 1017bp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 Sequence 115 AA;
 XX

Tue Nov 2 10:45:13 2004

us-10-802-574-4.rag

Qy 1 LSELDDRADALQAGASXFEKXSAKLRKXYWKYLK 35
Db 59 LSELDDRADALQAGASQFETSAKLRKXYWKYLK 93

Search completed: November 1, 2004, 18:04:03
Job time : 90 secs

Tue Nov 2 10:45:13 2004

us-10-802-574-4.ra1

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds
(without alignments)
99.035 Million cell updates/sec

Title: US-10-802-574-4

Sequence: 1 LSEIDRADALQAGASXFKSAALKKRWKXK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/aa/PCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	35	2	US-08-760-001-9
2	170	98.3	35	2	US-08-760-001-11
3	170	98.3	35	3	US-09-015-960-9
4	170	98.3	35	3	US-09-015-960-11
5	170	98.3	35	3	US-09-534-572-9
6	170	98.3	35	3	US-09-534-572-11
7	170	98.3	40	4	US-09-570-023-16
8	170	98.3	40	4	US-09-570-023-8
9	170	98.3	42	4	US-09-962-3608-9
10	170	98.3	62	2	US-08-760-001-8
11	170	98.3	62	2	US-09-015-960-8
12	170	98.3	62	3	US-09-534-572-8
13	170	98.3	116	1	US-08-409-373B-4
14	170	98.3	116	1	US-08-409-373B-4
15	170	98.3	116	1	US-08-393-985-16
16	170	98.3	116	3	US-08-621-018B-10
17	170	98.3	116	3	US-08-819-286-2
18	170	98.3	116	4	US-09-483-665-10
19	169	97.7	35	4	US-09-962-3608-4
20	168	97.1	82	4	US-08-621-018B-11
21	168	97.1	82	4	US-09-483-665-11
22	165	95.4	100	3	US-08-621-018B-6
23	165	95.4	100	4	US-09-483-665-6
24	165	95.4	103	1	US-08-409-373B-3
25	165	95.4	103	1	US-08-409-373B-3
26	165	95.4	103	3	US-08-621-018B-9
27	165	95.4	103	4	US-09-483-665-9

28	165	95.4	118	1	US-08-393-985-14	Sequence 14, Appl
29	165	95.4	347	4	US-09-513-783A-28	Sequence 28, Appl
30	165	95.4	347	4	US-09-430-656-30	Sequence 30, Appl
31	165	95.4	350	4	US-09-513-783A-30	Sequence 30, Appl
32	165	95.4	350	4	US-09-430-656-28	Sequence 28, Appl
33	162	93.6	35	4	US-09-962-3608-3	Sequence 3, Appl
34	106	61.3	56	3	US-08-819-286-5	Sequence 5, Appl
35	93	53.8	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	82	47.4	20	3	US-08-819-286-13	Sequence 13, Appl
37	82	47.4	71	4	US-09-621-976-5656	Sequence 5656, Ap
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39	82	47.4	102	1	US-08-409-373B-2	Sequence 2, Appl
40	82	47.4	102	3	US-08-621-018B-2	Sequence 2, Appl
41	82	47.4	102	4	US-08-483-665-2	Sequence 2, Appl
42	82	47.4	102	3	US-08-483-665-2	Sequence 2, Appl
43	76	43.9	141	3	US-08-621-018B-8	Sequence 8, Appl
44	76	43.9	141	4	US-09-483-665-8	Sequence 8, Appl
45	75	43.4	46	4	US-09-962-3608-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-760-001-9
Sequence 9, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-9
Query Match 98.3%, Score 170, DB 2, Length 35,
Best Local Similarity 94.3%, Pred. No. 3, 7e-19,
Matches 33, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 1 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 35

RESULT 2

US-08-760-001-11
Sequence 11, Application US/08760001

Patent No. 5962637

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,001

FILING DATE: Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/01279

FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-760-001-11

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 1 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 35

RESULT 3

US-09-015-960-9
Sequence 9, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-015-960-9
Query Match 98.3%; Score 170; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 3,7e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 1 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 35

RESULT 4

US-09-015-960-11
Sequence 11, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

Tue Nov 2 10:45:13 2004

us-10-802-574-4.ra1

Page 3

NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-11

Query Match 98.3%; Score 170; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 3.7e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLKRYWKNLK 35
Db 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

RESULT 5
US-09-534-572-9
Sequence 9, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-534-572-9

Query Match 98.3%; Score 170; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 3.7e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLKRYWKNLK 35
Db 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

RESULT 6
US-09-534-572-11
Sequence 11, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-11

Query Match 98.3%; Score 170; DB 3; Length 35;
Best Local Similarity 94.3%; Pred. No. 3.7e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLKRYWKNLK 35
Db 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

RESULT 7
US-09-570-022-16
Sequence 16, Application US/09570022
Patent No. 6573244
GENERAL INFORMATION:
APPLICANT: GORDON, RICHARD K.
APPLICANT: MOORAD, DEBORAH R.
APPLICANT: DOCTOR, BHUPENDRA P.
APPLICANT: GARCIA, GREGORY E.
TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
FILE REFERENCE: 38644-170531
CURRENT APPLICATION NUMBER: US/09/570,022
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/134,446
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-09-570-022-16

Query Match 98.3%; Score 170; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 4.3e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLX 35
DB 6 LSELDDRADALQAGASQFETSAKLRKRYWKNLX 40

RESULT 8
US-09-570-023-8
Sequence 8, Application US/09570023
Patent No. 6713444
GENERAL INFORMATION:
APPLICANT: GARCIA, GREGORY E.
APPLICANT: GORDON, RICHARD K.
APPLICANT: MOORAD, DEBORAH R.
APPLICANT: DOCTOR, BHUPENDRA P.
TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
FILE REFERENCE: 37833-20004.00
CURRENT APPLICATION NUMBER: US/09/570,023
CURRENT FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: VAMP2
US-09-570-023-8

Query Match 98.3%; Score 170; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 4.3e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLX 35
DB 6 LSELDDRADALQAGASQFETSAKLRKRYWKNLX 40

RESULT 9
US-09-962-360B-9
Sequence 9, Application US/09962360B
Patent No. 6762280
GENERAL INFORMATION:
/9

APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 9
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
US-09-962-360B-9

Query Match 98.3%; Score 170; DB 4; Length 42;
Best Local Similarity 94.3%; Pred. No. 4.6e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLX 35
DB 4 LSELDDRADALQAGASQFETSAKLRKRYWKNLX 38

RESULT 10
US-08-760-001-8
Sequence 8, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,693
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-8

Query Match 98.3%; Score 170; DB 2; Length 62;
Best Local Similarity 94.3%; Pred. No. 7.1e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 11
US-09-015-960-8
Sequence 8, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-8

Query Match 98.3%; Score 170; DB 3; Length 62;
Best Local Similarity 94.3%; Pred. No. 7.1e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 12
US-09-534-572-8
Sequence 8, Application US/09534572
Patent No. 6337386

GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-8

Query Match 98.3%; Score 170; DB 3; Length 62;
Best Local Similarity 94.3%; Pred. No. 7.1e-19;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 13
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5585240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: CELLULEREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 98.3%; Score 170; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.5e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 14
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5650280 5650280
Patent No. 5650280 5650240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Sellhauer, Jeffrey J.
TITLE OF INVENTION: CELLUBREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 98.3%; Score 170; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.5e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 15
US-08-393-985-16
Sequence 16, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-393-985-16

Query Match 98.3%; Score 170; DB 1; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.5e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Search completed: November 1, 2004, 18:19:41
Job time : 23.4375 secs

Tue Nov 2 10:45:13 2004

us-10-802-574-4.rapb

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds
(without alignments)
164,308 Million cell updates/sec

Title: US-10-802-574-4

Perfect score: 173
Sequence: 1 LSEIDRRADALQAGASXFEKSAALKRKYWKXK 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	42	US-09-962-360B-9	Sequence 9, Appl1
2	170	98.3	116	US-09-942-024-4	Sequence 4, Appl1
3	170	98.3	116	US-09-942-024-17	Sequence 17, Appl1
4	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
5	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
6	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
7	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
8	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
9	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
10	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
11	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
12	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
13	169	97.7	35	US-09-962-360B-4	Sequence 4, Appl1

14	168	97.1	82	US-10-357-028-11	Sequence 11, Appl1
15	168	97.1	114	US-09-942-024-19	Sequence 19, Appl1
16	168	97.1	114	US-09-942-024-19	Sequence 19, Appl1
17	168	97.1	114	US-10-261-161-14	Sequence 14, Appl1
18	168	97.1	114	US-10-261-161-14	Sequence 14, Appl1
19	165	95.4	100	US-10-357-028-6	Sequence 6, Appl1
20	165	95.4	103	US-10-357-028-6	Sequence 6, Appl1
21	165	95.4	117	US-10-467-595-27	Sequence 27, Appl1
22	165	95.4	118	US-09-942-024-96	Sequence 96, Appl1
23	165	95.4	118	US-09-942-024-96	Sequence 96, Appl1
24	165	95.4	118	US-10-261-161-10	Sequence 10, Appl1
25	165	95.4	347	US-10-100-9578-28	Sequence 28, Appl1
26	165	95.4	350	US-10-100-9578-30	Sequence 30, Appl1
27	165	95.4	365	US-09-293-670-52	Sequence 52, Appl1
28	162	93.6	35	US-09-962-360B-3	Sequence 3, Appl1
29	153	88.4	109	US-10-369-493-6364	Sequence 6364, Appl1
30	150	86.7	40	US-09-942-024-57	Sequence 57, Appl1
31	150	86.7	40	US-09-942-024-58	Sequence 58, Appl1
32	150	86.7	40	US-09-942-024-59	Sequence 59, Appl1
33	150	86.7	40	US-09-942-024-60	Sequence 60, Appl1
34	150	86.7	40	US-09-942-024-61	Sequence 61, Appl1
35	150	86.7	40	US-09-942-024-65	Sequence 65, Appl1
36	150	86.7	40	US-09-942-024-65	Sequence 65, Appl1
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42	150	86.7	40	US-10-261-161-82	Sequence 82, Appl1
43	150	86.7	40	US-10-261-161-83	Sequence 83, Appl1
44	150	86.7	40	US-10-261-161-84	Sequence 84, Appl1
45	150	86.7	40	US-10-261-161-85	Sequence 85, Appl1

ALIGNMENTS

RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmitt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoreceimyl-glycine
US-09-962-360B-9
Query Match 98.3%; Score 170; DB 10; Length 42;
Best Local Similarity 98.3%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 4 LSEIDRRADALQAGASXFEKSAALKRKYWKXK 35
1 LSEIDRRADALQAGASXFEKSAALKRKYWKXK 35
4 LSEIDRRADALQAGASXFEKSAALKRKYWKXK 38

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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 35
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 35
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
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; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-024-18

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 35
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 94

RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-4

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 35
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKRWXNLK 94

RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-17

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Tue Nov 2 10:45:13 2004

us-10-802-574-4.rapb

Page 3

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QY      1 LSELDDRADALQAGASQFETSAAKLKRYKWKX 35
      60 LSELDDRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 7
US-09-942-098-18
; Sequence 18, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-098-18

Query Match      98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LSELDDRADALQAGASQFETSAAKLKRYKWKX 35
      60 LSELDDRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 8
US-10-357-028-10
; Sequence 10, Application US/10357028
; Publication No. US20030180931A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Selhammer, Jeffrey J.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,028
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,665
; FILING DATE: Herewith
; APPLICATION NUMBER: 08/621,018
; FILING DATE: March 22, 1996
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-Cox, Diana
; REGISTRATION NUMBER: 33,102
; REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
```

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 433075
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

Query Match      98.3%; Score 170; DB 14; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LSELDDRADALQAGASQFETSAAKLKRYKWKX 35
      60 LSELDDRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 9
US-10-261-161-11
; Sequence 11, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-11

Query Match      98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 LSELDDRADALQAGASQFETSAAKLKRYKWKX 35
      60 LSELDDRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 10
US-10-261-161-12
; Sequence 12, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
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ORGANISM: Mus musculus
US-10-261-161-12

Query Match 98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
|||||
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 11
US-10-261-161-13
; Sequence 13, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays for Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-261-161-13

Query Match 98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
|||||
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 12
US-09-293-670-55
; Sequence 55, Application US/09293670
; Publication No. US20030190684A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Joseph
; APPLICANT: Lorens, James
; APPLICANT: Payan, Donald
; APPLICANT: Rossi, Alexander
; TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
; TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule
; FILE REFERENCE: A68104/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/293,670
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-293-670-55

Query Match 98.3%; Score 170; DB 10; Length 607;
Best Local Similarity 94.3%; Pred. No. 4.3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
|||||
|||||

DB 61 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 95

RESULT 13
US-09-962-360B-4
; Sequence 4, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9

; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc feature
; LOCATION: 17 and 20
; OTHER INFORMATION: Xaa at 17 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 ;
; OTHER INFORMATION: dimethylamino-4-methyl-coumarin-3-carboxamidomethyl)-cysteine
US-09-962-360B-4

Query Match 97.7%; Score 169; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
|||||
60 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35

RESULT 14
US-10-357-028-11
; Sequence 11, Application US/10357028
; Publication No. US20030180931A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Selthamer, Jeffrey J.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: CELLULIBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,028
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,665
; FILING DATE: Herewith
; APPLICATION NUMBER: 08/621,018
; FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-849-8886
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 606978
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 97.1%; Score 168; DB 10; Length 82;
Best Local Similarity 91.4%; Pred. No. 1,1e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 26 LSELDDRADALQAGASQFETSAAKLRKRYWKNMK 60

RESULT 15
US-09-942-024-19
Sequence 19, Application US/09942024
Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Estel
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Pret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 114
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-942-024-19

Query Match 97.1%; Score 168; DB 10; Length 114;
Best Local Similarity 91.4%; Pred. No. 1.5e-16;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 58 LSELDDRADALQAGASQFETSAAKLRKRYWKNMK 92

Search completed: November 1, 2004, 18:23:47
Job time : 69.0625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 18.125 Seconds
(without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDRADALQAGASXFEKSAKLRKYWKNLK 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	116	2 B38315	synapobrevin 2 -
2	170	98.3	116	2 UN0011	synapobrevin 2 -
3	170	98.3	116	2 B34288	synapobrevin 2 -
4	165	95.4	103	2 S35077	cellubrevin - rat
5	165	95.4	118	2 S52747	Vamp1 protein - hu
6	165	95.4	118	2 A38315	synapobrevin 1 -
7	165	95.4	118	2 A34288	vesicle-associated
8	165	95.4	120	2 A32146	vesicle-associated
9	155	89.6	125	2 S40153	synapobrevin - lo
10	153	88.4	109	2 T33239	synapobrevin SNB-
11	116	67.1	32	2 S35555	vesicle-associated
12	116	67.1	32	2 S35553	vesicle-associated
13	116	67.1	32	2 S35554	vesicle-associated
14	116	67.1	32	2 S35552	vesicle-associated
15	113	65.3	132	2 UC1522	synapobrevin 180f
16	113	65.3	132	2 UC1521	synapobrevin 180f
17	107	61.8	145	2 T21318	hypothetical prote
18	82	47.4	115	2 S62059	synapobrevin homo
19	81	46.8	123	2 S47654	integral membrane
20	76	43.9	121	2 T39073	synapobrevin homo
21	72	41.6	117	2 GNFF42	synapobrevin homo
22	71	41.0	1237	1 GNFF42	HIV-1 retropepsin
23	66	38.2	220	2 T00801	probable synapobrevin
24	62	35.8	60	2 D44088	homoeotic protein H
25	62	35.8	221	2 F84741	probable synapobrevin
26	60	34.7	175	2 D86180	hypothetical prote
27	57	33.9	251	2 S64927	probable membrane
28	57	33.9	663	2 H82731	glutaryl-7-ACA acy
29	56	32.4	229	2 F66180	hypothetical prote

30	56	32.4	240	2 T47589	synapobrevin-like
31	55	31.8	102	2 S44781	C30A5.4 protein -
32	55	31.8	102	2 T24909	hypothetical prote
33	54	31.2	219	2 T04630	synapobrevin homo
34	54	31.2	226	2 A97774	pepr protein (mpo
35	54	31.2	499	2 T18791	gamma-aminobutyric
36	53	30.6	259	2 A84377	cell division prot
37	53	30.6	450	2 A97740	hypothetical prote
38	53	30.6	450	2 A71678	probable response
39	52	30.1	855	2 T29775	hypothetical prote
40	52	30.1	1116	2 T42213	m-tomoxyn, isoform
41	51	29.5	210	2 T16595	hypothetical prote
42	51	29.5	1882	2 S73484	hypothetical prote
43	50	28.9	251	2 AD1145	cyclase Hsf homol
44	50	28.9	629	2 E64046	mismatch repair pr
45	50	28.9	958	2 S15566	pol protein - siml

ALIGNMENTS

RESULT 1
B38315
synapobrevin 2 - human
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C/Accession: B38315
R/Archer III, B.T.; Oerzelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A/Title: Structures and chromosomal localizations of two human genes encoding synapobrevin
A/Reference number: A38315; MUID:91009161; PMID:1976629
A/Accession: B38315
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-116 <ARC>
A/Cross-references: UNIPROT: P19065; GB:M36205; GB:J05611; NID:G338630; PIDN:AAA60604.1; I
C/Genetics:
A/Gene: GDB:SYB2; VAMP-2
A/Cross-references: GDB:125293; OMIM:185861
A/Map position: 17pter-17p12
C/Superfamily: synapobrevin
C/Keywords: membrane trafficking; transmembrane protein

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 2.3e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGASXFEKSAKLRKYWKNLK 35
DB 60 LSELDRADALQAGASXFEKSAKLRKYWKNLK 94

RESULT 2
UN0011
synapobrevin 2 - bovine
N/Alternate names: SNAP receptor
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: UN0011; S36811; S32363
R/Suedhof, T.C.; Baumeister, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A/Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A/Reference number: A93413; MUID:90180466; PMID:2560644
A/Accession: UN0011
A/Molecule type: mRNA
A/Residues: 1-116 <SUB>
A/Cross-references: UNIPROT: P19065; GB:X76199; NID:G433075; PIDN:CA451792.1; PID:G433076
A/Experimental source: UNIPROT: P19065; GB:X76199; NID:G433075; PIDN:CA451792.1; PID:G433076
R/Horiikawa, H.P.M.; Saleu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A/Title: A complex of rab3a, SNAP-25, VAMP/synapobrevin-2 and syntaxins in brain presyn
A/Reference number: S36811; MUID:93374072; PMID:8365494
A/Accession: S36811

vesicle-associated membrane protein 1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34288
R/Blot: L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1999
A/Title: Two vesicle-associated membrane protein genes are differentially expressed in
A/Reference number: A34288; MUID:89291844; PMID:2472388
A/Accession: A34288
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <ELP>
A/Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:G207628; PIDN:AAA42322.1;
C/Superfamily: synaptobrevin
C/Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 118;
Best Local Similarity 91.4%; Pred. No. 1.2e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35
DB 62 LSELDDRADALQAGASFEKSAKLRKYWKXK 96

RESULT 8

A32146
vesicle-associated membrane protein 1 - Pacific electric ray
C/Species: Torpedo californica (Pacific electric ray)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C/Accession: A32146
R/Trimble, W.S.; Cowan, D.M.; Scheller, R.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988
A/Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.
A/Reference number: A32146; MUID:88248054; PMID:3380805
A/Accession: A32146
A/Molecule type: mRNA
A/Residues: 1-120 <TRI>
A/Cross-references: UNIPROT:P13701; EMBL:J03777; NID:G213245; PIDN:AAA49286.1; PID:G2132
C/Superfamily: synaptobrevin
C/Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 120;
Best Local Similarity 91.4%; Pred. No. 1.3e-16;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35
DB 64 LSELDDRADALQAGASFEKSAKLRKYWKXK 98

RESULT 9

S40153
synaptobrevin - longfin squid
C/Species: Loligo pealeii (longfin squid)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S40153
R/Bommet, K.; Kistner, A.; Haselmann, E.; Betz, H.
submitted to the EMBL Data Library, August 1993
A/Description: Conservation of primary structure and clostridial neurotoxin cleavage site
A/Reference number: S40153
A/Accession: S40153
A/Molecule type: mRNA
A/Status: preliminary
A/Residues: 1-125 <BOM>
A/Cross-references: UNIPROT:P47194; EMBL:X74748; NID:G437855; PIDN:CAA52766.1; PID:G4378
C/Superfamily: synaptobrevin

Query Match 89.6%; Score 155; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 3.7e-15;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35

DB 69 LSELDDRADALQAGASFEKSAKLRKYWKXK 103

RESULT 10

T33239
synaptobrevin SNB-1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T33239
R/Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A/Description: The sequence of C. elegans cosmid T10H9.
A/Reference number: T21306
A/Accession: T33239
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-109 <GRE>

A/Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AAQ19234.1; GSPDB:GN00023; CESP:7
A/Experimental source: strain Bristol N2; clone T10H9
A/Genes: SNB-1; CESP:T10H9.4
A/Map position: 5
A/Introns: 39/3
C/Superfamily: synaptobrevin

Query Match 88.4%; Score 153; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 6.3e-15;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35
DB 52 LSELDDRADALQAGASFEKSAKLRKYWKXK 86

RESULT 11

S35555
vesicle-associated membrane protein 2 - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: S35555
R/Paternello, T.; Bazzelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A/Title: Neurotransmission and secretion.
A/Reference number: S35552; MUID:93354436; PMID:8350916
A/Accession: S35555
A/Molecule type: DNA
A/Residues: 1-32 <PAT>
A/Cross-references: UNIPROT:O7LZ64
C/Superfamily: synaptobrevin
C/Keywords: membrane trafficking; transmembrane protein

Query Match 67.1%; Score 116; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 3.9e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLR 27
DB 6 LSELDDRADALQAGASFEKSAKLR 32

RESULT 12

S35553
vesicle-associated membrane protein 1 - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 20-May-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S35553
R/Paternello, T.; Bazzelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A/Title: Neurotransmission and secretion.
A/Reference number: S35552; MUID:93354436; PMID:8350916
A/Accession: S35553
A/Molecule type: DNA

A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q7LZ65
C;Superfamily: synaptobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 3.9e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLR 27
DB 6 LSELDDRADALQAGASVFESSAKLR 32

RESULT 13

S35554
vesicle-associated membrane protein 2 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35554
R;Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q35619
C;Superfamily: synaptobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 3.9e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLR 27
DB 6 LSELDDRADALQAGASQFETSAKLR 32

RESULT 14

S35552

vesicle-associated membrane protein 1 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S35552
R;Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion.
A;Reference number: S35552; MUID:93354436; PMID:8350916
A;Accession: S35552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <PAT>
A;Cross-references: UNIPROT:Q9CXX2
C;Superfamily: synaptobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;
Best Local Similarity 92.6%; Pred. No. 3.9e-10;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLR 27
DB 6 LSELDDRADALQAGASQFESSAKLR 32

RESULT 15

JC1522

synaptobrevin isoform B - fruit fly (Drosophila melanogaster)

N;Alternate names: vesicle-associated membrane protein B
C;Species: Drosophila melanogaster
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: JC1522
R;Chin, A.C.; Burgees, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.

Gene 131, 175-181, 1993
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A;Reference number: JC1521; MUID:94010306; PMID:8406010

A;Accession: JC1522
A;Molecule type: DNA
A;Residues: 1-132 <CHI>
A;Cross-references: UNIPROT:P18489; GB:U14270; NID:G290281; PIDN:AAA28923.1; PID:G290282
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue 1
C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrevin
C;Genetics:
A;Gene: syb
A;Cross-references: FlyBase:FBgn0003660
A;Introns: 16/2; 128/1
C;Superfamily: synaptobrevin
C;Keywords: membrane protein; synaptic vesicle

Query Match 65.3%; Score 113; DB 2; Length 132;
Best Local Similarity 62.9%; Pred. No. 4.7e-09;
Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKQLK 35
DB 76 LSELGERADQLFGAGSGSEQAGKLRKQKQWAMMK 110

Search completed: November 1, 2004, 17:53:52
Job time: 19.125 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 / Search time 97.1875 Seconds
(without alignments)
207.209 Million cell updates/sec

Title: US-10-802-574-4
Perfect score: 173
Sequence: 1 LSELDRADALQAGASXFEKSAKLKRYKWNK 35

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TMMPARIES

Result No.	Score	Query Match	Length	DB	Description
1	170	98.3	81	2	Q8H2X7
2	170	98.3	114	2	Q6P835
3	170	98.3	114	2	AH61396
4	170	98.3	115	1	VAM2_HUMAN
5	170	98.3	115	1	VAM2_MOUSE
6	170	98.3	116	2	Q9BUC2
7	170	98.3	116	2	Q9NOY0
8	170	98.3	116	2	Q35619
9	170	98.3	116	2	AH02737
10	170	98.3	116	2	AH55105
11	170	98.3	116	2	BAC41125
12	170	98.3	135	2	Q9WUW2
13	170	98.3	142	2	Q8CHR4
14	170	98.3	113	1	VAM2_XENLA
15	168	97.1	114	2	AH60344
16	168	97.1	114	2	VAM3_HUMAN
17	165	96.4	103	1	VAM3_MOUSE
18	165	96.4	103	2	AAG42468
19	165	96.4	103	2	AAG60045
20	165	96.4	103	2	BAC34586
21	165	96.4	103	2	BAC34723
22	165	96.4	116	2	Q8CH14
23	165	96.4	117	2	Q8IVC9
24	165	96.4	117	2	Q85025
25	165	96.4	117	2	Q85FE3
26	165	96.4	117	2	AH57587
27	165	96.4	118	1	VAM1_HUMAN
28	165	96.4	118	1	VAM1_MOUSE
29	165	96.4	118	1	VAM1_RAT
30	165	96.4	118	1	BAC37551
31	165	96.4	120	1	SV5_TORCA

32	165	95.4	182	2	Q9CXX2	Q9CXX2 mus musculus
33	164	94.8	114	2	Q57345	Q57345 xenopus lae
34	163	94.2	102	2	Q61QK3	Q61QK3 brachydanio
35	163	94.2	102	2	AH71402	AH71402 brachydanio
36	163	94.2	119	2	Q6P8J3	Q6P8J3 brachydanio
37	163	94.2	119	2	AH59687	AH59687 brachydanio
38	161	93.1	100	2	Q9BRV4	Q9BRV4 homo sapien
39	160	92.5	110	2	Q75Z25	Q75Z25 brachydanio
40	160	92.5	110	2	AH59626	AH59626 brachydanio
41	160	92.5	112	2	Q57432	Q57432 fugu rubrip
42	156	90.2	86	2	Q6DLT0	Q6DLT0 lateolabrax
43	156	90.2	110	2	Q8T897	Q8T897 halocynthia
44	156	90.2	160	2	Q86FE0	Q86FE0 schistosoma
45	155	89.6	118	2	Q6DG11	Q6DG11 brachydanio

ALIGNMENTS

Result	ID	Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	Q8H2X7	170	98.3	2	81	33	0	2	0	0
2	Q6P835	170	98.3	2	114	33	0	2	0	0
3	AH61396	170	98.3	2	114	33	0	2	0	0
4	VAM2_HUMAN	170	98.3	1	115	33	0	2	0	0
5	VAM2_MOUSE	170	98.3	1	115	33	0	2	0	0
6	Q9BUC2	170	98.3	2	116	33	0	2	0	0
7	Q9NOY0	170	98.3	2	116	33	0	2	0	0
8	Q35619	170	98.3	2	116	33	0	2	0	0
9	AH02737	170	98.3	2	116	33	0	2	0	0
10	AH55105	170	98.3	2	116	33	0	2	0	0
11	BAC41125	170	98.3	2	135	33	0	2	0	0
12	Q9WUW2	170	98.3	2	142	33	0	2	0	0
13	Q8CHR4	170	98.3	2	113	33	0	2	0	0
14	VAM2_XENLA	170	98.3	1	113	33	0	2	0	0
15	AH60344	168	97.1	2	114	33	0	2	0	0
16	VAM3_HUMAN	168	97.1	2	114	33	0	2	0	0
17	VAM3_MOUSE	165	96.4	1	103	33	0	2	0	0
18	AAG42468	165	96.4	2	103	33	0	2	0	0
19	AAG60045	165	96.4	2	103	33	0	2	0	0
20	BAC34586	165	96.4	2	103	33	0	2	0	0
21	BAC34723	165	96.4	2	103	33	0	2	0	0
22	Q8CH14	165	96.4	2	116	33	0	2	0	0
23	Q8IVC9	165	96.4	2	117	33	0	2	0	0
24	Q85025	165	96.4	2	117	33	0	2	0	0
25	Q85FE3	165	96.4	2	117	33	0	2	0	0
26	AH57587	165	96.4	2	117	33	0	2	0	0
27	VAM1_HUMAN	165	96.4	1	118	33	0	2	0	0
28	VAM1_MOUSE	165	96.4	1	118	33	0	2	0	0
29	VAM1_RAT	165	96.4	1	118	33	0	2	0	0
30	BAC37551	165	96.4	1	118	33	0	2	0	0
31	SV5_TORCA	165	96.4	1	120	33	0	2	0	0

NCBI_TaxID=8364;
 OX [1]
 SEQUENCE FROM N.A.
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Hally J., Gills R.A.,
 RA Fanev J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywnicki M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC061396; AAH61396.1; -
 DR InterPro: IPR001388; SynaptoBrevin.
 DR Pfam: PF00957; SynaptoBrevin; 1.
 DR PRINTS: PR00219; SYNAPTOBREVIN.
 DR PRODOM: PD001229; SynaptoBrevin; 1.
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE: PS00932; V SNARE; 1.
 DR Hypothetical protein.
 KW SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;
 SQ
 Query Match 98.3%; Score 170; DB 2; Length 114;
 Best Local Similarity 94.3%; Pred. No. 8.8e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 35
 Db 58 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 92
 RESULT 3
 AAH61396 PRELIMINARY; PRT; 114 AA.
 AC AAH61396;
 DT 25-MAR-2004 (TrEMBLrel. 27, Created)
 DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC75977.
 GN MGC75977.
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 NCBI_TaxID=8364;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald W.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywnicki M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC061396; AAH61396.1; -
 DR InterPro: IPR001388; SynaptoBrevin.
 DR Pfam: PF00957; SynaptoBrevin; 1.
 DR PRINTS: PR00219; SYNAPTOBREVIN.
 DR PRODOM: PD001229; SynaptoBrevin; 1.
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE: PS00932; V SNARE; 1.
 DR Hypothetical protein.
 KW SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;
 SQ
 Query Match 98.3%; Score 170; DB 2; Length 114;
 Best Local Similarity 94.3%; Pred. No. 8.8e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 35
 Db 58 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 92
 RESULT 4
 VAM2 HUMAN STANDARD; PRT; 115 AA.
 AC P19065;
 DT 01-NOV-1990 (Ref. 16, Created)
 DT 01-NOV-1997 (Ref. 35, Last sequence update)
 DT 01-OCT-2004 (Ref. 45, Last annotation update)
 DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoBrevin 2).
 GN Name=VAMP2; Synonyms=SYB2;
 GN Homo sapiens (Human), and
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606; 9913;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA MEDLINE=9100916; PubMed=1976629;
 RA Archer B.T. III, Oezcelik T., Jahn R., Franke U., Suedhof T.C.;
 RT "Structures and chromosomal localizations of two human genes encoding
 RT synaptoBrevins 1 and 2.";
 RT J. Biol. Chem. 265:17267-17273(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Peripheral blood;
 RA Nabokina S.M., Lazo P.A., Molinedo F.;
 RT "Expression of VAMP genes in human neutrophils";
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RA Tarusio D., Zoraci K.G., Falbo V.;
 RT "Genomic structure of human SYB2 gene.";
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine; PubMed=2560644;
 RX MEDLINE=90180466; PubMed=2560644;
 RA Suedhof T.C., Baumeister M., Perin M.S., Jahn R.;
 RT "A synaptic vesicle membrane protein is conserved from mammals to
 RT Drosophila.";

RN Neuron 2:1475-1481(1989).
 RN (5)
 RP SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.
 RC SPECIES=Bovine;
 RX MEDLINE=93205116; PubMed=8455717;
 RA Scollner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,
 RA Germaines S., Tempst P., Rothman J.E.,
 RT "SNARE receptors implicated in vesicle targeting and fusion.";
 RT Nature 362:318-324(1993).
 RN (6)
 RP TISSUE SPECIFICITY.
 RC SPECIES=Human;
 RX MEDLINE=96332494; PubMed=8760387;
 RA Jagadeesh M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
 RA Grusovin J., Verkhran A., Cosgrove L., Alfacci A., Frenkel M.J.,
 RA Ward C.W.;
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25
 (synaptosomal-associated protein 25) A and B isoforms in addition to
 RT syntaxin 4 and synaptobrevins 1 and 2.";
 RT Biochem. J. 317:945-954(1996).
 RN (7)
 RP TOPOLOGY.
 RC SPECIES=Human;
 RX MEDLINE=95137000; PubMed=7835332;
 RA Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;
 RT "Transport route for synaptobrevin via a novel pathway of insertion
 RT into the endoplasmic reticulum membrane.";
 RT EMBO J. 14:217-223(1995).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.
 RC SPECIES=Human;
 RX MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;
 RA Hanson M.A., Stevens R.C.;
 RT "Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin
 RT type B at 2.0 A resolution.";
 RT Nat. Struct. Biol. 7:687-692(2000).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
 CC vesicles to their target membrane.
 CC -1- SUBUNIT: Interacts with VAMP and VAPB.
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
 CC vesicles.
 CC -1- TISSUE SPECIFICITY: Nervous system and skeletal muscle.
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M36205; AAA60604.1; JOINED.
 DR EMBL: M36201; AAA60604.1; JOINED.
 DR EMBL: M36202; AAA60604.1; JOINED.
 DR EMBL: M36203; AAA60604.1; JOINED.
 DR EMBL: M36204; AAA60604.1; JOINED.
 DR EMBL: M36205; AAA60604.1; JOINED.
 DR EMBL: A0225044; CAAL2385.1; -
 DR EMBL: AF135372; AAF15551.1; -
 DR EMBL: X76199; CA53792.1; -
 DR PIR: B38315; B38315.
 DR PIR: JN0011; JN0011.
 DR PDB: 1P83; X-ray; B=52-75, C=76-87.
 DR GeneW; HGNC:12643; VAMP2.
 DR MIM; 185881; -
 DR GO; GO:0005887; C:in integral to plasma membrane; TAS.
 DR InterPro; IPR001388; Synaptobrevin.
 DR Pfam; PF00957; Synaptobrevin; 1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; SYNAPTOBREVN; 1.
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.
 DR PROSITE; PS00892; V_SNARE; 1.

KW 3D-structure; Acetylation; Coiled coil; Direct protein sequencing;
 KM Multigene family; Synapse; Synaptosome; Transmembrane.
 FT INIT MET 0 93
 FT DOMAIN 1 93
 FT TRANSMEM 94 113
 FT DOMAIN 114 115
 FT MOD_RES 1 1
 FT DOMAIN 30 90
 FT SEQUENCE 115 AA; 12517 MW; 388B79F0D21AD81E CRC64;
 SQ
 Query Match 98.3%; Score 170; DB 1; Length 115;
 Best Local Similarity 94.3%; Pred. No. 8.9e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 LSELDRADALQAGSXFEXSAKTKRKYWKXNK 35
 59 LSELDRADALQAGSOFETSAKTKRKYWKXNK 93
 RESULT 5
 VAMP2 MOUSE STANDARD; PRT; 115 AA.
 ID VAMP2 MOUSE
 AC 064357;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
 GN Name=Vamp2; Synonyms=Synd2;
 OS Mus musculus (Mouse); and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090, 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Rat;
 RX MEDLINE=89281844; PubMed=2472388;
 RA Eiferink L.A., Trimble W.S., Scheffer R.H.;
 RT "Two vesicle-associated membrane protein genes are differentially
 RT expressed in the rat central nervous system.";
 RT J. Biol. Chem. 264:11061-11064(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Mouse;
 RX MEDLINE=98104125; PubMed=9430681;
 RA Martin L.B., Shewan A., Miller C.A., Gould G.W., James D.E.;
 RT "Vesicle-associated membrane protein 2 plays a specific role in the
 RT insulin-dependent trafficking of the facilitative glucose transporter
 RT GLUT4 in 3T3-L1 adipocytes.";
 RT J. Biol. Chem. 273:1444-1452(1998).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A
 RP AND SNAP25.
 RC SPECIES=Rat;
 RX MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;
 RA Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;
 RT "Crystal structure of a SNARE complex involved in synaptic exocytosis
 RT at 2.4 A resolution.";
 RT Nature 395:347-353(1998).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 28-93 IN COMPLEX WITH STX1A;
 RP CEPX1 AND SNAP25, AND NMR ANALYSIS.
 RC SPECIES=Rat;
 RX MEDLINE=21822661; PubMed=11832227;
 RA Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
 RA Suedhof T.C., Rizo J.;
 RT "Three-dimensional structure of the complexin/SNARE complex.";
 RT Neuron 33:409(2002).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A
 RP AND SNAP25.
 RC SPECIES=Rat;

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EX MEDLINE=2249607; PubMed=12496247; DOI=10.1074/jbc.M211889200;
RA Ernst J.A., Brunger A.T.;
RT "High resolution structure, stability, and synaptobrevin binding of a
RL truncated neuronal SNARE complex."
CC J. Biol. Chem. 278:8630-8636(2003).
CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
CC vesicles to their target membrane.
CC -1- SUBUNIT: Interacts with VAMP and VAPB (By similarity). Part of the
CC SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC complex binds to CPLX1.
CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC vesicles.
CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC expression is seen in the brain as compared to the spinal cord.
CC -1- SIMILARITY: Belongs to the synaptobrevin family.
CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M24105; AAA42321.1; -
DR EMBL; U60150; AAB03463.1; -
DR PIR; B34288; B34288.
DR PDB; 1KTI; X-ray; A=26-91.
DR PDB; 1N7S; X-ray; A=26-88.
DR PDB; 1SFC; X-ray; A/E/I=1-95.
DR WGI; MGI:1313277; Vamp2.
DR RGD; 3949; Vamp2.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; SYNAPTOBREVN.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS00892; V-SNARE; 1.
DR PROSITE; PS00892; V-SNARE; 1.
DR 3D-structure; Acetylation; Coiled coil; Multigene family;
DR Polymorphism; Synapse; Synaposome; Transmembrane.
DR INIT MET 0
DR DOMAIN 0
DR TRANSMEM 94 113
FT 114 115 Vesicular (potential).
FT MOD RES 1 1 N-acetylserine (By similarity).
FT DOMAIN 30 90 v-SNARE coiled-coil homology.
FT VARIANT 110 110 I -> II.
FT VARIANT 111 111 V -> I.
FT HELIX 28 87
SQ SEQUENCE 115 AA; 12559 MW; EA40D6291ABF0BC CRC64;

Query Match 98.3%; Score 170; DB 1; Length 115;
Best Local Similarity 94.3%; Pred. No. 8, 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXNLK 35
Db 59 LSELDDRADALQAGASQFETSAKLRKYWKXNLK 93

RESULT 6
ID Q9BUC2 PRELIMINARY; PRT; 116 AA.
AC Q9BUC2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).
GN Name:VAMP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Testis;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marisna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalao D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villing J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.A., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinsky W.I., Skalski V., Smallov D.B., Schmeich A., Schein U.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002737; AAH02737.3; -
DR EMBL; BC019608; AAH19608.1; -
DR EMBL; BC033870; AAH33870.1; -
DR HSR; Q9WUR2; 1SFC.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; SYNAPTOBREVN; 1.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS00892; V-SNARE; 1.
SQ SEQUENCE 116 AA; 12663 MW; 9CDD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXNLK 35
Db 60 LSELDDRADALQAGASQFETSAKLRKYWKXNLK 94

RESULT 7
ID Q9NOY0 PRELIMINARY; PRT; 116 AA.
AC Q9NOY0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE VAMP-2 (Rhesus macaque).
GN Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;

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OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF240769; AAF64476.1; -.
DR HSSP: Q9WUW2; ISPC.
DR InterPro: IPR001388; Synaptoobrevin.
DR Pfam: PF00857; Synaptoobrevin.1.
DR PRINTS: PR00219; SYNAPTOBREVN.
DR PRODOM: PD001229; Synaptoobrevin.1.
DR PROSITE: PS00417; SYNAPTOBREVN; 1.
DR PROSITE: PS50892; V_SNAPE; 1.
SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match          98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 8
ID 035619 PRELIMINARY; PRT; 116 AA.
AC 035619;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-2004 (TREMBLrel. 26, Last annotation update)
DE Vesicle associated membrane protein 2.
GN Name=Vamp2; Synonyms=mvamp-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen S.K., Doerre S., Corley R.B.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF007168; AAB62931.1; -.
DR PIR: S35554; S35554.
DR HSSP: Q9WUW2; ISPC.
DR MGD: MGI:1313277; Vamp2.
DR GO: GO:0030141; C:secretory granule; IDA.
DR GO: GO:0030672; C:synaptic vesicle membrane; IDA.
DR GO: GO:0042589; C:cyzomgranule membrane; IDA.
DR GO: GO:0005516; F:calmodulin binding; IDA.
DR GO: GO:0005543; F:phospholipid binding; IDA.
DR GO: GO:0000149; F:SNARE binding; IDA.
DR GO: GO:0017156; P:calcium ion-dependent exocytosis; IDA.
DR GO: GO:0016083; P:regulation of exocytosis; IDA.
DR InterPro: IPR001388; Synaptoobrevin.
DR Pfam: PF00957; Synaptoobrevin.1.
DR PRINTS: PR00219; SYNAPTOBREVN.
DR PRODOM: PD001229; Synaptoobrevin.1.
DR PROSITE: PS00417; SYNAPTOBREVN; 1.
DR PROSITE: PS50892; V_SNAPE; 1.
SQ SEQUENCE 116 AA; 12677 MW; 4E1DD056B5409D0A CRC64;

Query Match          98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

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RESULT 9
ID AAH02737 PRELIMINARY; PRT; 116 AA.
AC AAH02737;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Vesicle-associated membrane protein 2 (Synaptoobrevin 2).
GN VAMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Koriy K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.O., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002737; AAH02737.3; -.
SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match          98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 10
ID AAH55105 PRELIMINARY; PRT; 116 AA.
AC AAH55105;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Vesicle-associated membrane protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feing J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL EMBL, BC055105; AAHS5105.1; - 4A0DD056B5409D0A CRC64;
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;
 Query Match 98.3%; Score 170; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 9e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Cy 1 LSEIDRADALQAGASFEKSAKLRKRYWKXK 35
 Db 60 LSEIDRADALQAGASFEKSAKLRKRYWKXK 94
 RESULT 11
 ID BAC41125 PRELIMINARY; PRT; 116 AA.
 AC BAC41125;
 DT 14-APR-2004 (Tremblrel. 27, Created)
 DT 14-APR-2004 (Tremblrel. 27, Last sequence update)
 DT 14-APR-2004 (Tremblrel. 27, Last annotation update)
 DE 15 days embryo brain cDNA, RIKEN full-length enriched library,
 DE clone/G630012G02 product:unclassified, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sun N., Ishi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Obara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Yamamatsu M., Hayashizaki Y.;
 RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AK090178; BAC41125.1; -
 DR EMBL, AK090178; BAC41125.1; -
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;
 Query Match 98.3%; Score 170; DB 2; Length 116;
 Best Local Similarity 94.3%; Pred. No. 9e-17;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Cy 1 LSEIDRADALQAGASFEKSAKLRKRYWKXK 35
 Db 60 LSEIDRADALQAGASFEKSAKLRKRYWKXK 94
 RESULT 12
 ID Q9WUM2 PRELIMINARY; PRT; 135 AA.
 AC Q9WUM2;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Vesicle associated membrane protein 2B.
 GN Name=vamp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99297576; PubMed=10371166;
 RA Mandic R., Lowe A.W.;
 RT "Characterization of an alternatively spliced isoform of rat vesicle
 RT associated membrane protein-2 (VAMP-2).";
 RL FEBS Lett. 451:209-213(1999).
 DR EMBL, AJ131104; CAB43809.1; -
 DR InterPro, IPR001388; Synapc-obrevin.
 DR Pfam, PF00957; Synapc-obrevin; 1.
 DR PRINTS, PR00219; Synapc-obrevin;
 DR ProDom, PD001229; Synapc-obrevin; 1.

DR PROSITE, PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE, PS50892; V_SNAKE; 1.
 SQ SEQUENCE 135 AA; 14509 MW; F37D14A87BDAB1F6 CRC64;
 Query Match 98.3%; Score 170; DB 2; Length 135;
 Best Local Similarity 94.3%; Pred. No. 1,1e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
 |||
 DB 60 LSELDDRADALQAGASQFETSAAKLKRYWKNLK 94
 |||

RESULT 13
 ID Q8CHRA PRELIMINARY; PRT; 142 AA.
 AC Q8CHRA;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Vamp2 protein (Fragment).
 OS Name=Vamp2;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stopleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
 Rana S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Paley J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 Krzywinski M.I., Skalske U., Smalios D.E., Scherch A., Schein J.E.,
 Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 DB EMBL, BC039745; AAA39745.1; -;
 DR HSSP; Q9KWM2; ISFC.
 DR MGD; MGI:131377; Vamp2.
 DR GO; GO:0030141; C:secretory granule; IDA.
 DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.
 DR GO; GO:0042589; C:zymogen granule membrane; IDA.
 DR GO; GO:0005516; F:calmodulin binding; IDA.
 DR GO; GO:0005543; F:phospholipid binding; IDA.
 DR GO; GO:0000149; F:SNARE binding; IDA.
 DR GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.
 DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.
 DR InterPro: IPR001388; SynaptoBrevin.
 DR Pfam: PF00957; SynaptoBrevin. 1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; SYNAPTOBREVN.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS50892; V_SNAKE; 1.

FT NON_TER 1 1
 SQ SEQUENCE 142 AA; 15313 MW; F1B0C9C9B495B776 CRC64;
 Query Match 98.3%; Score 170; DB 2; Length 142;
 Best Local Similarity 94.3%; Pred. No. 1,1e-16;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
 |||
 DB 86 LSELDDRADALQAGASQFETSAAKLKRYWKNLK 120
 |||

RESULT 14
 ID VAM2_XENLA STANDARD; PRT; 113 AA.
 AC P47193;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoBrevin 2)
 DE (SVB1).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OX Xenopodidae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang X.-H., Poo M.-M.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 32-113 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=95324415; PubMed=7601005;
 RA Knecht A.K., Good P.J., Dawid I.B., Harland R.M.;
 RT "Dorsal-ventral patterning and differentiation of noggin-induced
 neural tissue in the absence of mesoderm.";
 RL Development 121:1927-1935(1995).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
 vesicles to their target membrane.
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
 vesicles.
 CC -1- SIMILARITY: Belongs to the synaptoBrevin family.
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AF035017; AAB88138.1; -;
 DR EMBL; U16801; AAA81376.1; -;
 DR HSSP; P19065; IPR3.
 DR InterPro: IPR001388; SynaptoBrevin.
 DR Pfam; PF00957; SynaptoBrevin. 1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; SYNAPTOBREVN.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 DR Acetylacton; Coiled coil; Multigene family; Synapse; Synaposome;
 KW Transmembrane.
 FT INIT MET 0
 FT DOMAIN 1 91 By similarity.
 FT TRANSMEM 92 110 Cytoplasmic (Potential).
 FT TRANSMEM 92 110 Anchor for type IV membrane protein
 FT TRANSMEM 92 110 (Potential).
 FT DOMAIN 111 113 Vesicular (Potential).
 FT MOD RES 1 88 N-acetylsuccinyl (By similarity).
 FT DOMAIN 1 88 V-SNARE coiled-coil homology.
 SQ SEQUENCE 113 AA; 12341 MW; 6EC6C937B29BC6AB CRC64;

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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 / Search time 108 Seconds
(without alignments)
139.506 Million cell updates/sec

Title: US-10-802-574-9

Perfect score: 221

Sequence: 1 XGJSELDPRADALQAGASQ.....TSAAKLRKXWKNLKGSGC 42

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358725299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	99.5	42	5	AA015163
2	181	81.9	40	4	AA050301
3	181	81.9	40	4	AA048582
4	181	81.9	54	3	AA039482
5	181	81.9	115	7	AA057598
6	181	81.9	115	7	AA057612
7	181	81.9	115	7	AA0560831
8	181	81.9	115	7	AA057606
9	181	81.9	115	7	AA0560829
10	181	81.9	115	7	AA057600
11	181	81.9	115	7	AA057604
12	181	81.9	115	7	AA057596
13	181	81.9	115	7	AA057602
14	181	81.9	115	7	AA057610
15	181	81.9	115	7	AA057592
16	181	81.9	115	7	AA057594
17	181	81.9	115	7	AA057614
18	181	81.9	115	7	AA057608
19	181	81.9	115	7	AA030104
20	181	81.9	116	2	AA043435
21	181	81.9	116	3	AA048823
22	181	81.9	116	5	AA043681
23	181	81.9	116	6	AA0476220
24	181	81.9	116	6	AA036664
25	181	81.9	116	7	AA001719

26	181	81.9	116	7	AA001718	Abw01718	Mouse VAM
27	181	81.9	116	7	AA001705	Abw01705	Human VAM
28	181	81.9	116	7	AA089011	Adg89011	Bovine sy
29	181	81.9	116	8	AA097006	Adm97006	Mouse VAM
30	181	81.9	116	8	AA097007	Adm97007	Bovine VA
31	181	81.9	116	8	AA097005	Adm97005	Human VAM
32	181	81.9	368	3	AA043843	AA043843	Amino act
33	181	81.9	368	3	AA090403	AA090403	Rat VAMP-
34	181	81.9	608	3	AA043845	AA043845	Amino act
35	181	81.9	609	3	AA090406	AA090406	Rat VAMP-
36	179	81.0	82	3	AA088244	AA088244	Xenopus s
37	179	81.0	82	7	AA089012	AA089012	Xenopus s
38	179	81.0	114	7	AA001720	AA001720	Frog VAMP
39	179	81.0	114	8	AA097008	AA097008	Frog VAMP
40	177	80.1	37	2	AA086822	AA086822	VAMP 1sot
41	177	80.1	62	2	AA086821	AA086821	VAMP 1sot
42	176	79.6	35	2	AA086824	AA086824	VAMP 1sot
43	176	79.6	100	2	AA004182	AA004182	Cellubrev
44	176	79.6	100	3	AA088240	AA088240	Human cel
45	176	79.6	100	4	AA000250	AA000250	SNARE hom

ALIGNMENTS

RESULT 1	AA015163	standard; peptide; 42 AA.
ID	AA015163	
XX	AA015163	
AC	02-SEP-2002	(first entry)
DT		
XX		
DE	Clostridial neurotoxin protease substrate peptide 2.	
XX		
KM	Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FBET;	
KM	fluorescence resonant energy transfer assay; quenched-signal;	
KM	clostridial neurotoxin detection; food.	
XX		
OS	Unidentified.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	1
FT	Cleavage-site	/note="N-fluoresceinyl-glycine"
FT		20.21
FT		/note="The peptide is cleaved between these two residues by the clostridial neurotoxin"
XX		
FN	WC020225284-A2.	
XX		
PD	28-MAR-2002.	
XX		
PF	25-SEP-2001; 2001WO-US030188.	
XX		
PR	25-SEP-2000; 2000US-0235050P.	
XX		
PA	(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.	
XX		
PI	Schmidt JT, Stafford RG;	
XX		
DR	WPI; 2002-499829/53.	
XX		
PT	Substrate useful in e.g. an assay for the protease activity of	
PT	clostridial neurotoxin, comprises modified peptide or protein.	
XX		
PS	Claim 24; Page 15; 48pp; English.	
XX		
CC	The invention comprises clostridial neurotoxin substrate peptides which	
CC	can serve as fluorescence resonant energy transfer assay (FBET) or	
CC	quenched-signal substrates in assays for the proteolytic activities of	
CC	clostridial neurotoxins. The invention further comprises Clostridium	
CC	botulinum neurotoxin substrate peptides that can serve as immobilised	
CC	substrates (i.e. bound to a solid phase) in assays for the proteolytic	

activities of clostridial neurotoxins. The clostridial (including the Clostridium botulinum) neurotoxin substrate peptides are useful for detecting the presence of clostridial neurotoxins in a sample (e.g. food or an environmental sample). The present amino acid sequence represents a clostridial neurotoxin substrate peptide of the invention

Sequence 42 AA:

Query Match 99.5%; Score 220; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.5e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGLSELDPRADALQAGASQFETSAKLKKRYWKNLKGQC 42
DB 2 GGLSELDPRADALQAGASQFETSAKLKKRYWKNLKGQC 42

RESULT 2
AAB50301
ID AAB50301 standard; peptide; 40 AA.

XX AAB50301;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

XX VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;
XX tetanus neurotoxin; buforinin.

XX Unidentified.

XX WO200069891-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-US013215.

XX 17-MAY-1999; 99US-0134446P.

XX (USGA) US DEPT OF THE ARMY.

XX Gordon RK, Moorad DR, Doctor BP, Garcia GE;

XX WPI; 2001-025001/03.

XX Novel Previn compounds useful for inhibiting the protease activity of Botulinum B and tetanus toxins.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence was investigated in the search for Botulinum toxin inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity of BttxB and tetanus neurotoxins were isolated. Previns may be used to construct compounds such as buforinins

XX Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKKRYWKNL 38
DB 6 LSELDDRADALQAGASQFETSAKLKKRYWKNL 40

RESULT 3

XX AAB48582
ID AAB48582 standard; peptide; 40 AA.

XX AAB48582;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

XX Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;
XX antibacterial; VAMP2; synaptobrevin.

XX Unidentified.

XX WO200069895-A2.

XX 23-NOV-2000.

XX 11-MAY-2000; 2000WO-US012909.

XX 14-MAY-1999; 99US-0134216P.

XX (USGA) US DEPT OF THE ARMY.

XX Garcia GE, Gordon RK, Moorad DR, Doctor BP;

XX WPI; 2001-102250/11.

XX Novel peptides capable of inhibiting the enzymatic activity of Botulinum toxin B, and Tetanus neurotoxins useful for preventing or treating toxic poisoning such as Botulinum toxin and tetanus poisoning.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence is one of a number of peptide or peptide-like compounds, designated buforinins, which inhibit the enzymatic activity of Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforinins are useful for treating Botulinum or tetanus intoxication by administering a composition comprising a buforin to the subject prior to the contact with BttxB or tetanus intoxication. Antibodies specific for buforinins are useful for detecting buforinins by forming immunocomplexes. The buforinins have improved circulatory half-life, solubility, resistance to degradation and interaction with the active site of the toxin

XX Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKKRYWKNL 38
DB 6 LSELDDRADALQAGASQFETSAKLKKRYWKNL 40

RESULT 4
AAB39482
ID AAB39482 standard; protein; 54 AA.

XX AAB39482;

XX 02-FEB-2001 (first entry)

XX Gene 49 human secreted protein homologous amino acid sequence #141.

XX Human; secreted protein; diagnosis; cytoprotective; immunosuppressive;
XX nocitropic; neuroprotective; antiviral; antiallergic; hepatotropic;
XX antidiabetic; antiinflammatory; antiviral; anticonvulsant;
XX antibacterial; antifungal; antiparasitic; cardiant; gene therapy;
XX food additive; preservative; chromosome identification; cancer;
XX female reproductive system disorder; immune disorder; wound healing;
XX cardiovascular disorder; neurological disease; infectious disease;
XX infection.

XX Bos taurus.

XX WO200058340-A2.

PD		05-OCT-2000.	
PF			
XX	23-MAR-2000;	2000MO-US007724.	
PR	26-MAR-1999;	99US-0126510P.	
PR	07-JAN-2000;	2000US-0174850P.	
PA	(HUMA-)	HUMAN GENOME SCI INC.	
PI	Rosen CA,	Ruben SM, Komatsoulis G;	
DR	WPI; 2000-	594638/56.	
XX			
PT	Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.		
PS	Disclosure; Page 390;	391pp; English.	
XX			
CC	The polynucleotide sequences given in AAC74337 to AAC74386 encode the human secreted proteins given in AAB39402 to AAB39451. AAB39452 to AAB39444 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include:		
CC	cystostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer; vulnerrary; anticoagulant; antibacterial; antifungal; antiparasitic; and cardiant.		
CC	The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotide are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast and/or ovarian cancer. They are also useful in the gene therapy of breast and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular disorders; (d) wound healing; (e) neurological diseases; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in the exemplification of the present invention.		
CC			
XX			
SQ	Sequence 54 AA;		
	Query Match	81.9%; Score 181; DB 3; Length 54;	
	Best Local Similarity	100.0%; Pred. No. 2.8e-17;	
	Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	4 LSELDLRADALDAGASQFETSAAKTKRKXWKXIKL 38 		
DB	20 ISELDDRADALDAGASQFETSAAKTKRKXWKXNLK 54 		
RESULT 5			
ID	ADEB57598 standard; protein; 115 AA.		
AC	ADEB57598;		
DT	29-JAN-2004 (first entry)		
XX			
DZ	Human Protein P19065, SEQ ID NO 3460.		
XX			
KW	Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.		
OS	Homo sapiens.		
XX			
FN	WO2003016475-A2.		
XX			

PD
Z/FEB-2003.
PF 14-AUG-2002; 2002MO-USO25765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX FI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; P19065.PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Claim 1, Page; 1017bp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury ('Chung'), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 115 AA;

Query Match	Bt. %:	Score 181;	DB ?;	Length 115;
Best Local Similarity	100.0%	Pred. No. 6.6e-17;	Mismatches 0;	Gaps 0
Matches	35;	Conservative 0;	Indels 0;	

Db 4 LSEIDBRADALQAGASGFETSAAKLKKRYWKNLK 38
 59 LSELDDRADA.LQGAGSGFETSAALKKRYWKNLTK 93

RESULT 6
ADES7612 ID ADE57612 standard, protein; 115 AA.
AC ADES7612;
DT 29-JAN-2004 (first entry)
DE Rat Protein Q64357, SEQ ID NO 3474.
KW Raf; pain; neuronal tissue; gene therapy; spinal segmental nerve injury/
chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
XX

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OS Rattus norvegicus.
PN WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; Q64357.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 115 AA;
XX
XX Query Match 81.9%; Score 181; DB 7; Length 115;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-17;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 LSELDDRADALQAGASQFETSAKTKRKYWKXK 38
DB 59 LSELDDRADALQAGASQFETSAKTKRKYWKXK 93
RESULT 7
ADE60831
ID ADE60831 standard; protein; 115 AA.
XX
XX ADE60831;
XX
XX 29-JAN-2004 (first entry)
XX Human Protein P19065, SEQ ID NO 6743.
XX

```

```

XX XX Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P19065.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 115 AA;
XX
XX Query Match 81.9%; Score 181; DB 7; Length 115;
XX Best Local Similarity 100.0%; Pred. No. 6.6e-17;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 LSELDDRADALQAGASQFETSAKTKRKYWKXK 38
DB 59 LSELDDRADALQAGASQFETSAKTKRKYWKXK 93
RESULT 8
ADE57606
ID ADE57606 standard; protein; 115 AA.
XX

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AC	AD557606;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human Protein P19065; SEQ ID NO 3468.
XX	
KW	Human; pain; neuronal tissue; gene therapy;
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
XX	spared nerve injury; SNI; Chung.
OS	Homo sapiens.
PN	WO2003016475-A2.
PD	
XX	
PF	27-FEB-2003.
PR	
XX	
PR	14-AUG-2002; 2002MO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P.
XX	
PR	01-NOV-2001; 2001US-0346382P.
XX	
PA	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GHEO) GEN HOSPITAL CORP.
XX	(FARB) BAYER AG.
PI	
DR	Woelf C, D'urso D, Befort K, Costigan M;
XX	
DR	WPI; 2003-268312/26.
XX	
DR	GENBANK; P19065.
PT	
XX	
PT	New composition comprising two or more isolated polypeptides, useful for
XX	preparing a medicament for treating pain in an animal.
PS	
PS	Claim 1; Page; 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC	therapy). The sequence presented is a human protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 115 AA;
Query Match	81.9%; Score 181; DB 7; Length 115;
Best Local Similarity	100.0%; Pred. No. 6,66-17;
Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4	LSLDDRRADALDAGASQFTSAAKRKRYWNK 38
59	LSLLDDRADALDAGASQFTSAAKRKRYWNK 93

Query Match	Best Local Similarity	Matches	Score 181;	DB 7;	Length 115;
81.9%;	100.0%;	0;	Pred. NO. 6.6e-17;	0;	Gaps 0;
35;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY 4 LSELDRADALQAGASQFETSAKLKRYKWNKX 38
DB 59 LSELDRADALQAGASQFETSAKLKRYKWNKX 93

RESULT 10
ADES7600
ID ADE57600 standard; protein; 115 AA.

AC ADE57600;

DT 29-JAN-2004 (first entry)

DE Rat Protein Q64357, SEQ ID NO 3462.

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN W02003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WC-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

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DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6,6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDRADALQAGASQFETSAKLKRYKWNKX 38
DB 59 LSELDRADALQAGASQFETSAKLKRYKWNKX 93

RESULT 11
ADES7604
ID ADE57604 standard; protein; 115 AA.

AC ADE57604;

DT 29-JAN-2004 (first entry)

DE Rat Protein Q64357, SEQ ID NO 3466.

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN W02003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WC-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

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DR GENBANK; Q64357.

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DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

DR GENBANK; Q64357.

CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 115 AA;
SQ Query Match 81.9%; Score 181; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 4 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 38
Db 59 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 93
RESULT 12
ID ADE57596 standard; protein; 115 AA.
XX ADE57596;
AC 29-JAN-2004 (first entry)
XX DE Rat Protein Q64357, SEQ ID NO 3458.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX PN 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENEANK; Q64357.
DR New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 115 AA;
Cy Query Match 81.9%; Score 181; DB 7; Length 115;
Db Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 4 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 38
Db 59 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 93
RESULT 13
ID ADE57602 standard; protein; 115 AA.
XX ADE57602;
AC 29-JAN-2004 (first entry)
XX DT Human Protein P19065, SEQ ID NO 3464.
XX DE Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX PN 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENEANK; P19065.
DR New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antipeptides. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

XX Query Match 81.9%; Score 181; DB 7; Length 115;

XX Best Local Similarity 100.0%; Pred. No. 6,6e-17;

XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38
DB 59 LSELDPRADALQAGASQFETSAKLRKRYWKXK 93

RESULT 14

XX ID ADE57610 standard; protein; 115 AA.

XX AC ADE57610;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P19065, SEQ ID NO 3472.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002MO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GENO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'Urso D, Befort K, Costigan M;

XX WP1; 2003-268312/26.

XX DR GENBANK; P19065.

XX PT New composition comprising two or more isolated polypeptides, useful for

XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antipeptides. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 115 AA;

XX Query Match 81.9%; Score 181; DB 7; Length 115;

XX Best Local Similarity 100.0%; Pred. No. 6,6e-17;

XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38
DB 59 LSELDPRADALQAGASQFETSAKLRKRYWKXK 93

RESULT 15

XX ID ADE57592 standard; protein; 115 AA.

XX AC ADE57592;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein Q64357, SEQ ID NO 3454.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002MO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GENO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'Urso D, Befort K, Costigan M;

XX WP1; 2003-268312/26.

XX DR GENBANK; Q64357.

XX PT New composition comprising two or more isolated polypeptides, useful for

XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence

Tue Nov 2 10:45:15 2004

us-10-802-574-9.ra1

Page 1

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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 28.125 Seconds
(Without alignments)
99.035 Million cell updates/sec

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Perfect score: 221
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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	99.5	42	4	US-09-962-360B-9
2	181	81.9	35	2	US-08-760-001-11
3	181	81.9	35	3	US-09-015-960-11
4	181	81.9	35	3	US-09-534-572-11
5	181	81.9	40	4	US-09-570-022-16
6	181	81.9	40	4	US-09-570-023-8
7	181	81.9	116	1	US-08-409-373B-4
8	181	81.9	116	1	US-08-409-373B-4
9	181	81.9	116	1	US-08-393-985-16
10	181	81.9	116	3	US-08-621-018B-10
11	181	81.9	116	3	US-08-621-018B-10
12	181	81.9	116	3	US-09-483-665-10
13	179	81.0	82	4	US-08-621-018B-11
14	179	81.0	82	4	US-09-483-665-11
15	177	80.1	35	2	US-08-760-001-9
16	177	80.1	35	3	US-09-015-960-9
17	177	80.1	35	3	US-09-534-572-9
18	177	80.1	62	2	US-08-760-001-8
19	177	80.1	62	3	US-09-015-960-8
20	177	80.1	62	3	US-09-534-572-8
21	176	79.6	100	3	US-08-621-018B-6
22	176	79.6	100	4	US-09-483-665-6
23	176	79.6	103	1	US-08-409-373B-3
24	176	79.6	103	1	US-08-409-373B-3
25	176	79.6	103	3	US-08-621-018B-9
26	176	79.6	103	4	US-09-483-665-9
27	176	79.6	347	4	US-09-513-783A-28

28	176	79.6	347	4	US-09-430-656-30	Sequence 30, Appl
29	176	79.6	350	4	US-09-513-783A-30	Sequence 30, Appl
30	176	79.6	350	4	US-09-430-656-28	Sequence 28, Appl
31	170	76.9	35	4	US-09-962-360B-4	Sequence 4, Appl
32	169	76.5	35	4	US-09-962-360B-3	Sequence 3, Appl
33	165	74.7	118	1	US-08-393-985-14	Sequence 14, Appl
34	117	52.9	56	3	US-08-819-286-5	Sequence 5, Appl
35	104	47.1	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	93	42.1	20	3	US-08-819-286-13	Sequence 13, Appl
37	89	40.3	71	4	US-09-621-976-5656	Sequence 5656, Ap
38	88	39.8	86	4	US-09-513-999C-5451	Sequence 5451, Ap
39	88	39.8	102	1	US-08-409-373B-2	Sequence 2, Appl
40	88	39.8	102	1	US-08-409-373B-2	Sequence 2, Appl
41	88	39.8	102	3	US-08-621-018B-2	Sequence 2, Appl
42	88	39.8	102	4	US-09-483-665-2	Sequence 2, Appl
43	82.5	37.3	46	4	US-09-962-360B-10	Sequence 10, Appl
44	76	34.4	141	3	US-08-621-018B-8	Sequence 8, Appl
45	76	34.4	141	4	US-09-483-665-8	Sequence 8, Appl

ALIGNMENTS

```
RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-Fluoresceinyl-glycine
US-09-962-360B-9

Query Match          99.5%: Score 220; DB 4; Length 42;
Best Local Similarity 100.0%: Pred. No. 1.4e+22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2  GGLSELDRADALQAGASQFETSAKLKRYWKXNLKG3GC 42
Db      2  GGLSELDRADALQAGASQFETSAKLKRYWKXNLKG3GC 42

RESULT 2
US-08-760-001-11
; Sequence 11, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-11

Query Match 81.9%; Score 181; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
DB 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

RESULT 3
US-09-015-960-11
Sequence 11, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-11

Query Match 81.9%; Score 181; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
DB 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

RESULT 4
US-09-534-572-11
Sequence 11, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-574-572-11

Query Match 81.9%; Score 181; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38
Db 1 LSELDDRADALQAGASQFETSAKLKRYWKNLK 35

RESULT 5
US-09-570-022-16
Sequence 16, Application US/09570022
Patent No. 6573344
GENERAL INFORMATION:
APPLICANT: GORDON, RICHARD K.
APPLICANT: MOORAD, DEBORAH R.
APPLICANT: DOCTOR, BHUPENDRA P.
APPLICANT: GARCIA, GREGORY E.
TITLE OF INVENTION: PREVIOUS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
FILE REFERENCE: 38644-170531
CURRENT APPLICATION NUMBER: US/09/570.022
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/134,446
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
US-09-570-022-16

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38
Db 6 LSELDDRADALQAGASQFETSAKLKRYWKNLK 40

RESULT 6
US-09-570-023-8
Sequence 8, Application US/09570023
Patent No. 6713444
GENERAL INFORMATION:
APPLICANT: GARCIA, GREGORY E.
APPLICANT: GORDON, RICHARD K.
APPLICANT: MOORAD, DEBBIE R.
APPLICANT: DOCTOR, BHUPENDRA P.
TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
FILE REFERENCE: 37833-20004.00
CURRENT APPLICATION NUMBER: US/09/570.023
CURRENT FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-570-023-8

Query Match 81.9%; Score 181; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38
Db 6 LSELDDRADALQAGASQFETSAKLKRYWKNLK 40

RESULT 7
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5585240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: CELLUBREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 81.9%; Score 181; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38
Db 60 LSELDDRADALQAGASQFETSAKLKRYWKNLK 94

RESULT 8
US-08-409-373B-4
Sequence 4, Application US/08409373B
Patent No. 5650280
Patent No. 5650280 5585240
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: CELLUBREVIN HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,373B
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0029 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0195
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: X76199
US-08-409-373B-4

Query Match 81.9%; Score 181; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 9
US-08-393-985-16
Sequence 16, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-393-985-16

Query Match 81.9%; Score 181; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 10
US-08-621-018B-10
Sequence 10, Application US/08621018B
Patent No. 6060239
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Selthamer, Jeffrey J.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: CELLULREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,018B
FILING DATE: March 22, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0029-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 433075
US-08-621-018B-10

Query Match 81.9%; Score 181; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

Db 60 LSELDPRADALQAGASQFETSAKLKRYWKNLK 94

RESULT 11

US-08-819-286-2

Sequence 2, Application US/08819286

Patent No. 6169074

GENERAL INFORMATION:

APPLICANT: Montcal, Mauricio

TITLE OF INVENTION: PEPTIDE INHIBITORS OF NEUROTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/819,286

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,599

FILING DATE: 18-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07349/005001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-819-286-2

Query Match 81.9%; Score 181; DB 3; Length 116;

Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LSELDPRADALQAGASQFETSAKLKRYWKNLK 38

Db 60 LSELDPRADALQAGASQFETSAKLKRYWKNLK 94

RESULT 12

US-09-483-665-10

Sequence 10, Application US/09483665

Patent No. 6534275

GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.

APPLICANT: Hawkins, Phillip R.

APPLICANT: Selhamer, Jeffrey J.

APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: CELLUBREVIN HOMOLOGS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/483,665

FILING DATE: Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,018

FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373

FILING DATE: March 23, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-Cox, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: PF-0029-2 DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-849-8886

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI 433075

US-09-483-665-10

Query Match 81.9%; Score 181; DB 4; Length 116;

Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 LSELDPRADALQAGASQFETSAKLKRYWKNLK 38

Db 60 LSELDPRADALQAGASQFETSAKLKRYWKNLK 94

RESULT 13

US-08-621-018B-11

Sequence 11, Application US/08621018B

Patent No. 6060239

GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.

APPLICANT: Hawkins, Phillip R.

APPLICANT: Selhamer, Jeffrey J.

APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: CELLUBREVIN HOMOLOGS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,018B

FILING DATE: March 22, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/409,373

FILING DATE: March 23, 1995

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0029-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 606978
US-08-621-01B-11

Query Match 81.0%; Score 179; DB 3; Length 82;
Best Local Similarity 97.1%; Pred. No. 9,1e-17;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

Db 26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

RESULT 14
US-09-483-665-11
Sequence 11, Application US/09483665
Patent No. 6534275
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: CELLULREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pasteo Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483,665
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,018
FILING DATE: March 22, 1996
APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-849-8886
TELEFAX: 650-855-0555
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK

CLONE: GI 606978
US-09-483-665-11

Query Match 81.0%; Score 179; DB 4; Length 82;
Best Local Similarity 97.1%; Pred. No. 9,1e-17;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

Db 26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

RESULT 15
US-08-760-001-9
Sequence 9, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:
APPLICANT: Shore, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-9

Query Match 80.1%; Score 177; DB 2; Length 35;
Best Local Similarity 97.1%; Pred. No. 6,6e-17;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38
1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

Db 1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

Search completed: November 1, 2004, 18:19:42
Job time : 29.125 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 82.875 Seconds

(without alignments)
164.308 Million cell updates/sec

Title: US-10-802-574-9

Perfect score: 221 USGSEIDDPADALQAGASQ.....TSAAKLKRYKWKIKGGGC 42

Sequence: 1 XGGSEIDDPADALQAGASQ.....TSAAKLKRYKWKIKGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues 1370721

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

Result No.	Score	Query Match	Length	ID	Description
1	220	99.5	42	US-09-962-360B-9	Sequence 9, Appl1
2	181	81.9	116	US-09-942-024-4	Sequence 4, Appl1
3	181	81.9	116	US-09-942-024-17	Sequence 17, Appl1
4	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
5	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
6	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
7	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
8	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
9	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
10	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
11	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
12	181	81.9	116	US-09-942-024-18	Sequence 18, Appl1
13	179	81.0	82	US-10-357-028-11	Sequence 11, Appl1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl1
15	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl1
16	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl1
17	176	79.6	100	14	US-10-357-028-6	Sequence 6, Appl1
18	176	79.6	103	14	US-10-357-028-9	Sequence 9, Appl1
19	176	79.6	347	14	US-10-100-957A-28	Sequence 28, Appl1
20	176	79.6	350	14	US-10-100-957A-30	Sequence 30, Appl1
21	176	79.6	365	10	US-09-293-670-52	Sequence 52, Appl1
22	172	77.8	117	16	US-10-467-595-27	Sequence 27, Appl1
23	172	77.8	118	10	US-09-942-024-36	Sequence 36, Appl1
24	172	77.8	118	10	US-09-942-024-36	Sequence 36, Appl1
25	172	77.8	118	10	US-09-942-024-36	Sequence 36, Appl1
26	170	76.9	35	10	US-09-962-360B-3	Sequence 3, Appl1
27	169	76.5	35	10	US-09-962-360B-3	Sequence 3, Appl1
28	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
29	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
30	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
31	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
32	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
33	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
34	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
35	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
36	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl1
37	159	71.9	109	14	US-10-369-493-6364	Sequence 6364, Appl1
38	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
39	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
40	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
41	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
42	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
43	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
44	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl1
45	157	71.0	104	10	US-09-942-024-57	Sequence 57, Appl1

ALIGNMENTS

RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication NO. US2003007685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmitt, James J.
; APPLICANT: Staifford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid:
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SNP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
; US-09-962-360B-9
Query Match 99.5%; Score 220; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-024-18

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-4

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-17

Query Match
Best Local Similarity 100.0%; Score 181; DB 10; Length 116;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ORGANISM: Mus musculus
US-10-261-161-12

Query Match 81.9%; Score 181; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNK 38
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNK 94

RESULT 11
US-10-261-161-13

Sequence 13, Application US/10261161
Publication No. US20040072270A1
GENERAL INFORMATION:
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Steward, Lance E.
TITLE OF INVENTION: Cell-based Fluorescence Resonance Energy
Transfer (FRET) Assays For Clostridial Toxins
FILE REFERENCE: P-AK 4804
CURRENT FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13
LENGTH: 116
TYPE: PRT
ORGANISM: Bos taurus
US-10-261-161-13

Query Match 81.9%; Score 181; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNK 38
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNK 94

RESULT 12
US-09-293-670-55

Sequence 55, Application US/09293670
Publication No. US20030190684A1
GENERAL INFORMATION:
APPLICANT: Fisher, Joseph
APPLICANT: Lorens, James
APPLICANT: Payan, Donald
APPLICANT: Rossi, Alexander
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in
Cellular Parameters and to Screen Small Molecule
FILE REFERENCE: A68104/DB/RMS/DAV
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 55
LENGTH: 607
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-293-670-55

Query Match 81.9%; Score 181; DB 10; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNK 38
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNK 94

DB 61 LSELDPRADALQAGASQFETSAKLKRYWKXNK 95

RESULT 13
US-10-357-028-11

Sequence 11, Application US/10357028
Publication No. US20030180931A1
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Selhammer, Jeffrey J.
TITLE OF INVENTION: CELLULREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 29-Jan-2003
APPLICATION NUMBER: US/10/357,028
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/483,665
FILING DATE: Herewith
APPLICATION NUMBER: 08/621,018
FILING DATE: March 22, 1996
APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-849-8886
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 606978
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-357-028-11

Query Match 81.0%; Score 179; DB 14; Length 82;
Best Local Similarity 97.1%; Pred. No. 5.1e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNK 38
DB 26 LSELDPRADALQAGASQFETSAKLKRYWKXNK 60

RESULT 14
US-09-942-024-19

Sequence 19, Application US/09942024
Publication No. US20030143650A1
GENERAL INFORMATION:
APPLICANT: Steward, Lance E.
APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger


```

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-024-19

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Query Match      81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      4 LSEIDDRADALQAGASQFETSAKLKRRKYYWKNLK 38
      |||
Db      58 LSEIDDRADALQAGASQFETSAKLKRRKYYWKNLK 92

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RESULT 15

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US-09-942-098-19
; Sequence 19, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-098-19

```

```

Query Match      81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 LSEIDDRADALQAGASQFETSAKLKRRKYYWKNLK 38
      |||
Db      58 LSEIDDRADALQAGASQFETSAKLKRRKYYWKNLK 92

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Search completed: November 1, 2004, 18:23:48
 Job time : 83.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 21.75 Seconds
(without alignments)
185.798 Million cell updates/sec

Title: US-10-802-574-9
Perfect score: 221
Sequence: 1 XGGLSELDPRADALQAGASQ.....TSAAKLKRYWKXNLKGGGC 42

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	81.9	116	2 B38315	synaptobrevin 2 -
2	181	81.9	116	2 JN0011	synaptobrevin 2 -
3	181	81.9	116	2 B34288	synaptobrevin 2 -
4	176	79.6	103	2 S35077	cellubrevin - rat
5	172	77.8	118	2 S52747	Vamp1 protein - hu
6	172	77.8	118	2 A36315	synaptobrevin 1 -
7	172	77.8	120	2 A32146	vesicle-associated
8	165	74.7	118	2 A34288	vesicle-associated
9	161	72.9	125	2 S40153	synaptobrevin - 1c
10	159	71.9	109	2 T33239	synaptobrevin SNB
11	127	57.5	32	2 S35555	vesicle-associated
12	127	57.5	32	2 S35554	vesicle-associated
13	123	55.7	32	2 S35552	synaptobrevin 1aof
14	119	53.8	132	2 JCI522	synaptobrevin 1aof
15	119	53.8	152	2 JCI521	vesicle-associated
16	116	52.5	32	2 S35553	vesicle-associated
17	113	51.1	145	2 T21318	hypothetical prote
18	92	41.6	223	2 S47654	integral membrane
19	82	37.1	115	2 S62059	synaptobrevin homo
20	75	33.9	121	2 T39073	synaptobrevin homo
21	72	32.6	117	2 S31250	synaptobrevin homo
22	72	32.6	220	2 T00801	probable synaptob
23	70	31.7	1237	1 GNFF42	HIV-1 retropepin
24	68	30.8	60	2 D44088	homeotic protein H
25	68	30.8	221	2 F64741	probable synaptob
26	66	29.9	175	2 D86180	hypothetical prote
27	64	29.0	251	2 AD1145	cyclase H1sf homo
28	62.5	28.3	515	2 S59811	vacuolar segregati
29	62	28.1	229	2 F86180	hypothetical prote

30	62	28.1	251	2 AD1504	cyclase H1sf homo
31	59	26.7	609	2 S64927	probable membrane
32	59	26.7	251	2 AB9500	glutamine-fructose
33	58	26.2	102	2 S47881	C30A5.4 protein -
34	58	26.2	102	2 T24909	hypothetical prote
35	58	26.2	450	2 A97740	hypothetical prote
36	58	26.2	450	2 A71678	hypothetical prote
37	57	25.8	210	2 T16595	petr protein limpo
38	57	25.8	226	2 A97774	succinate dehydrog
39	56.5	25.6	588	2 G82118	synaptobrevin homo
40	56	25.3	219	2 T04630	synaptobrevin-like
41	56	25.3	240	2 T47589	anthranilate synth
42	56	25.3	454	2 A11641	glutaryl-7-ACA acy
43	56	25.3	663	2 H82731	carboxylesterase (
44	55	24.9	565	2 S10367	transducer protein
45	55	24.9	788	2 T44262	

ALIGNMENTS

RESULT 1
B38315
synaptobrevin 2 - human
C/Species: Homo sapiens (man)
C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C/Accession: B38315
R/Archer IIL, B.T.; Oezcelik, T.; Jahn, R.; Franke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A/Title: Structures and chromosomal localizations of two human genes encoding synaptobrevin
A/Reference number: A38315; MUID:91009161; PMID:1976629
A/Accession: B38315
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-116 <ARC>
A/Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:G338630; PIDN:AAA60604.1; J
C/Genetic:
A/Gene: GDB:SYB2; VAMP-2
A/Cross-references: GDB:125293; OMIM:185881
A/Map position: 17pter-17p12
C/Superfamily: synaptobrevin
C/Keywords: membrane trafficking; transmembrane protein

Query Match 81.9%; Score 181; DB 2; Length 116;
Best Local Similarity 100.0%; Pred.No. 1.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 4 LSELDDPRADALQAGASQFETSAKLRKYWKXNLK 38
Db 60 LSELDDPRADALQAGASQFETSAKLRKYWKXNLK 94
RESULT 2
JN0011
synaptobrevin 2 - bovine
N/Alternate names: SNAP receptor
C/Species: Bos primigenius tauros (cattle)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: JN0011; S36811; S32363
R/Suedhof, T.C.; Baumeister, W.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A/Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A/Reference number: A93413; MUID:90180466; PMID:2560644
A/Accession: JN0011
A/Molecule type: mRNA
A/Residues: 1-116 <SUB>
A/Cross-references: UNIPROT:P19065; GB:X76199; NID:G433075; PIDN:CAA53792.1; PID:G433076
A/Experimental source: brain
R/Horikawa, H.P.M.; Saito, H.; Ishizuka, T.; Sakine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A/Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A/Reference number: S36811; MUID:93374072; PMID:8365494
A/Accession: S36811

A/Molecule type: mRNA
A/Residues: 'X',48-79 <HOR>
A/Experimental source: brain
R/Scellner, T.; Whiteheart, S.W.; Brunner, M.; Erijuntunt-Bromage, H.; Gezomanos, S.; Tem
Nature 362, 318-324, 1993
A/Title: SNAP receptors implicated in vesicle targeting and fusion.
A/Reference number: S32360; MUID:93205116; PMID:8455717
A/Accession: S32363
A/Molecule type: protein
A/Residues: 31-47,'X',49-55,'X',57-59,67-82 <SOE>
A/Experimental source: brain
C/Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.
C/Superfamily: synaptobrevin
C/Keywords: acetylated amino end, membrane trafficking, transmembrane protein
F/2-116/Product: synaptobrevin 2 #status predicted <MAT>
F/95-114/Domain: transmembrane #status predicted <TM>
F/2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 81.9%; Score 181; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
60 LSEIDRADALQAGASQFETSAKLRKRYWKXK 94

RESULT 3
B34288
synaptobrevin 2 - rat
N/Alternate names: vesicle-associated membrane protein 2
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
C/Accession: B34288; S27125
R/Elferink, L.A.; Trimble, W.S.; Scheller, R.H.
J. Biol. Chem. 264, 11061-11064, 1989
A/Title: Two vesicle-associated membrane protein genes are differentially expressed in t
A/Reference number: A34288; MUID:89291844; PMID:2472388
A/Accession: B34288
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <ELF>
A/Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:G207626; PIDN:AAA42321.1;
R/Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; Dasgupta, B.R
Nature 359, 832-835, 1992
A/Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt
A/Reference number: S27125; MUID:93063293; PMID:1331807
A/Accession: S27125
A/Molecule type: protein
A/Residues: 77-99,'X',101 <SCH>
C/Superfamily: synaptobrevin
C/Keywords: membrane protein; membrane trafficking; synaptic vesicle

Query Match 81.9%; Score 181; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
60 LSEIDRADALQAGASQFETSAKLRKRYWKXK 94

Db 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
60 LSEIDRADALQAGASQFETSAKLRKRYWKXK 94

RESULT 4
S35077
cellubrevin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S35077
R/Memaron, H.T.; Usharyov, Y.A.; Edelmann, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R
Nature 364, 346-349, 1993
A/Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy
A/Reference number: S35077; MUID:93323976; PMID:8332193
A/Accession: S35077

A/Molecule type: mRNA
A/Residues: 1-103 <MCN>
A/Cross-references: UNIPROT:Q64271; GB:S63830; NID:G368482; PIDN:AAAB27554.1; PID:G368483
C/Superfamily: synaptobrevin

Query Match 79.6%; Score 176; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 7.6e-15;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
47 LSEIDRADALQAGASQFETSAKLRKRYWKXK 81

Db 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
47 LSEIDRADALQAGASQFETSAKLRKRYWKXK 81

RESULT 5
S52747
Vamp1 protein - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S52747
R/Gough, K.H.; Verkhrulyan, A.; Cosgrove, L.; Frenkel, M.U.; Ward, C.W.
Submitted to the EMBL Data Library, December 1994
A/Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.
A/Reference number: S52747
A/Accession: S52747
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <GOU>
A/Cross-references: UNIPROT:P23763; EMBL:Z48924; NID:G758107; PIDN:CAA8760.1; PID:G75810
C/Superfamily: synaptobrevin

Query Match 77.8%; Score 172; DB 2; Length 118;
Best Local Similarity 94.3%; Pred. No. 2.9e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
62 LSEIDRADALQAGASQFETSAKLRKRYWKXK 96

Db 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
62 LSEIDRADALQAGASQFETSAKLRKRYWKXK 96

RESULT 6
A38315
synaptobrevin 1 - human
C/Species: Homo sapiens (man)
C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C/Accession: A38315
R/Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 265, 17267-17273, 1990
A/Title: Structures and chromosomal localizations of two human genes encoding synaptobrev
A/Reference number: A38315; MUID:9100916; PMID:1976629
A/Accession: A38315
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-118 <ARC>
A/Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:G338623; PIDN:AAA60603.1; P
C/Genetics: A38315
A/Gene: GDB:SYB1; VAMP-1
A/Cross-references: GDB:125292; OMIM:185880
A/Map position: 12p-12p
C/Superfamily: synaptobrevin
C/Keywords: membrane trafficking; transmembrane protein

Query Match 77.8%; Score 172; DB 2; Length 118;
Best Local Similarity 94.3%; Pred. No. 2.9e-15;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
62 LSEIDRADALQAGASQFETSAKLRKRYWKXK 96

Db 4 LSEIDRADALQAGASQFETSAKLRKRYWKXK 38
62 LSEIDRADALQAGASQFETSAKLRKRYWKXK 96

RESULT 7
A32146

vesicle-associated membrane protein 1 - Pacific electric ray
 C/Species: Torpedo californica (Pacific electric ray)
 C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
 C/Accession: A32146
 R/Trimble, W.S.; Cowan, D.W.; Scheller, R.H.
 Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988
 A/Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.
 A/Reference number: A32146; PMID:88248054; PMID:3380805
 A/Accession: A32146
 A/Molecule type: mRNA
 A/Residues: 1-120 <TRI>
 A/Cross-references: UNIPROT:P13701; EMBL:J03777; NID:G213245; PIDN:AAA9286.1; PID:G2132
 C/Superfamily: synaptobrevin
 C/Keywords: membrane protein

Query Match 77.8%; Score 172; DB 2; Length 120;
 Best Local Similarity 94.3%; Pred. No. 3e-15; Mismatches 1; Indels 0; Gaps 0;
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38
 |||||
 DB 64 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 98

RESULT 8

A34288
 vesicle-associated membrane protein 1 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 01-Jun-1990 #sequence_revision 01-Jun-1990 #text_change 09-Jul-2004
 C/Accession: A34288
 R/Eiferink, L.A.; Trimble, W.S.; Scheller, R.H.
 U. Biol. Chem. 264, 11061-11064, 1989
 A/Title: Two vesicle-associated membrane protein genes are differentially expressed in v
 A/Reference number: A34288; MUID:89291844; PMID:2472388
 A/Accession: A34288
 A/Status: Preliminary
 A/Molecule type: mRNA
 A/Residues: 1-118 <EUF>
 A/Cross-references: UNIPROT:O63666; GB:M24104; GB:U04827; NID:G207628; PIDN:AAA42322.1;
 C/Superfamily: synaptobrevin
 C/Keywords: membrane protein

Query Match 74.7%; Score 165; DB 2; Length 118;
 Best Local Similarity 91.4%; Pred. No. 2.4e-14; Mismatches 2; Indels 0; Gaps 0;
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38
 |||||
 DB 62 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 96

RESULT 9

S40153
 synaptobrevin - longfin squid
 C/Species: Loligo pealeii (longfin squid)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S40153
 R/Bowmer, K.; Kistner, A.; Hasemann, E.; Betz, H.
 Submitted to the EMBL Data Library, August 1993
 A/Description: Conservation of primary structure and clostridial neurotoxin cleavage sit
 A/Reference number: S40153
 A/Accession: S40153
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-125 <BOW>
 A/Cross-references: UNIPROT:P47194; EMBL:X74748; NID:9437855; PIDN:CAA22766.1; PID:94378
 C/Superfamily: synaptobrevin

Query Match 72.9%; Score 161; DB 2; Length 125;
 Best Local Similarity 85.7%; Pred. No. 8.6e-14; Mismatches 3; Indels 0; Gaps 0;
 Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38

DB :|||||
 69 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 103

RESULT 10

T33239
 synaptobrevin SNB-1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T33239
 R/Greco, T.; Bradshaw, H.; O'Brien, D.
 Submitted to the EMBL Data Library, May 1998
 A/Description: The sequence of C. elegans cosmid T10H9.
 A/Reference number: Z21306
 A/Accession: T33239
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-109 <GRE>
 A/Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AA19234.1; GSPDB:GN00023; CESP:
 A/Experimental source: strain Bristol N2; clone T10H9
 C/Genetics:
 A/Genes: SNB-1; CESP:T10H9.4
 A/Map position: 5
 A/Intons: 39/3
 C/Superfamily: synaptobrevin

Query Match 71.9%; Score 159; DB 2; Length 109;
 Best Local Similarity 85.7%; Pred. No. 1.4e-13; Mismatches 3; Indels 0; Gaps 0;
 Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38
 |||||
 DB 52 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 86

RESULT 11

S35555
 vesicle-associated membrane protein 2 - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S35555
 R/Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
 Nature 364, 581-582, 1993
 A/Title: Neurotransmission and secretion.
 A/Reference number: S35552; MUID:93354436; PMID:8350916
 A/Accession: S35555
 A/Molecule type: DNA
 A/Residues: 1-32 <PAT>
 A/Cross-references: UNIPROT:Q7L264
 C/Superfamily: synaptobrevin
 C/Keywords: membrane trafficking; transmembrane protein

Query Match 57.5%; Score 127; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.8e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLK 30
 |||||
 DB 6 LSELDLRADALQAGASQFETSAAKLK 32

RESULT 12

S35554
 vesicle-associated membrane protein 2 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C/Accession: S35554
 R/Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
 Nature 364, 581-582, 1993
 A/Title: Neurotransmission and secretion.
 A/Reference number: S35552; MUID:93354436; PMID:8350916
 A/Accession: S35554
 A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-32 <PAT>
A:Cross-references: UNIPROT:O35619
C:Superfamily: synaptobrevin

Query Match 57.5%; Score 127; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKTKR 30
DB 6 LSELDDRADALQAGASQFETSAKTKR 32

RESULT 13
S35552
vesicle-associated membrane protein 1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S35552
R:Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A:Title: Neurotransmission and secretion.
A:Reference number: S35552; PMID:93354436; PMID:8350916
A:Accession: S35552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-32 <PAT>
A:Cross-references: UNIPROT:Q9CXX2
C:Superfamily: synaptobrevin

Query Match 55.7%; Score 123; DB 2; Length 32;
Best Local Similarity 96.3%; Pred. No. 1.9e-09;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKTKR 30
DB 6 LSELDDRADALQAGASQFETSAKTKR 32

RESULT 14
JC1522
synaptobrevin isoform B - fruit fly (Drosophila melanogaster)
N:Alternate names: vesicle-associated membrane protein B
C:Species: Drosophila melanogaster
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C:Accession: JC1522
R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A:Reference number: JC1521; PMID:94010306; PMID:8406010
A:Accession: JC1522
A:Molecule type: DNA
A:Residues: 1-132 <CHI>
A:Cross-references: UNIPROT:P18489; GB:U14270; NID:G290281; PIDN:AAA28923.1; PID:G290282
A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobre
C:Genetics:
A:Gene: syb
A:Cross-references: FlyBase:FBgn0003660
A:introns: 16/2; 128/1
C:Superfamily: synaptobrevin
C:Keywords: membrane protein; synaptic vesicle

Query Match 53.8%; Score 119; DB 2; Length 132;
Best Local Similarity 65.7%; Pred. No. 2.8e-08;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKTKR 38
DB 76 LSELGERADOLEGASOSFOQAGKTKRKQWANNK 110

RESULT 15
JC1521
synaptobrevin isoform A - fruit fly (Drosophila melanogaster)
N:Alternate names: vesicle-associated membrane protein A
C:Species: Drosophila melanogaster
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C:Accession: JC1521; UN0012
R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.
Gene 131, 175-181, 1993
A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene
A:Reference number: JC1521; PMID:94010306; PMID:8406010
A:Accession: JC1521
A:Molecule type: DNA

A:Residues: 1-152 <CHI>
A:Cross-references: UNIPROT:P18489; GB:U14270; NID:G290281; PIDN:AAA28924.1; PID:G290283
A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue
R:Suedhof, T.C.; Baumeister, M.; Perin, M.S.; Jahn, R.
Neuron 2, 1475-1481, 1989
A:Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.
A:Reference number: A93413; PMID:90180466; PMID:2560644
A:Accession: UN0012
A:Molecule type: mRNA
A:Residues: 1-92, 'F', 94-152 <SUE>
C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobre
C:Genetics:
A:Gene: syb
A:Cross-references: FlyBase:FBgn0003660
A:introns: 16/2; 128/1
C:Superfamily: synaptobrevin
C:Keywords: synaptic vesicle; transmembrane protein
F:111-130/Domain: transmembrane #status predicted <TRMM>

Query Match 53.8%; Score 119; DB 2; Length 152;
Best Local Similarity 65.7%; Pred. No. 3.3e-08;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKTKR 38
DB 76 LSELGERADOLEGASOSFOQAGKTKRKQWANNK 110

Search completed: November 1, 2004, 17:53:52
Job time : 21.75 secs


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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
DR InterPro; IPR001388; Synaplobrevin.
DR Pfam; PF00957; Synaplobrevin; 1.
DR PRINTS; PR00219; SYNAPLOBREV.
DR PRODOM; PD001229; Synaplobrevin; 1.
DR PROSITE; PS00417; SYNAPLOBREVIN; 1.
DR PROSITE; PS50892; V_SNAARE; 1.
KM Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 81.9%; Score 181; DB 2; Length 114;
Best Local Similarity 100.0%; Pred.No. 7.7e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38
DB 58 LSELDPRADALQAGASQFETSAKLRKRYWKXK 92

RESULT 3
AAH61396 PRELIMINARY; PRT; 114 AA.
AC AAH61396;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MG075977.
GN MG075977.
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus; Silurana.
CX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
KM Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

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RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
KM Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 81.9%; Score 181; DB 2; Length 114;
Best Local Similarity 100.0%; Pred.No. 7.7e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38
DB 58 LSELDPRADALQAGASQFETSAKLRKRYWKXK 92

RESULT 4
VAMP2 HUMAN STANDARD; PRT; 115 AA.
AC P19065;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaplobrevin 2).
GN Name=VAMP2; Synonyms=SYB2;
OS Homo sapiens (Human); and
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606, 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=91009161; PubMed=1976629;
RA Archer B.T. III, Ozercevik T., Jahn R., Francke U., Suedhof T.C.;
RT "Structures and chromosomal localizations of two human genes encoding
RT synaplobrevins 1 and 2."
RL J. Biol. Chem. 265:17267-17273 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Peripheral blood;
RA Nabokina S.M., Lazo P.A., Mollinedo F.;
RT "Expression of VAMP genes in human neutrophils."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Blood;
RA Tarsicio D., Zoraghi K.G., Falbo V.;
RT "Genomic structure of human SYB2 gene."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=90180466; PubMed=2560644;
RA Suedhof T.C., Baumeister M., Perin M.S., Jahn R.;
RT "A synaptic vesicle membrane protein is conserved from mammals to
RT Drosophila."

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RX MEDLINE=22499607; PubMed=12496247; DOI=10.1074/jbc.M211899200;
RA Ernst J.A., Brunker A.T.;
RT "High resolution structure, stability, and synaptobrevin binding of a
RL truncated neuronal SNARE complex."
RL J. Biol. Chem. 278:8630-8636(2003).
CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
CC vesicles to their target membrane.
CC -1- SUBUNIT: Interacts with VAMP and VAPB (By similarity). Part of the
CC SNARE core complex containing SNAP25, VAMP2 and STX1A. This
CC complex binds to CGLX1.
CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC vesicles.
CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level
CC expression is seen in the brain as compared to the spinal cord.
CC -1- SIMILARITY: Belongs to the synaptobrevin family.
CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M24105; AAA4321.1; -
DR EMBL; U60150; AAB03463.1; -
DR PIR; B34288; B34288.
DR PDB; 1K1L; X-ray; A=26-91.
DR PDB; 1N7S; X-ray; A=26-88.
DR PDB; 1SFC; X-ray; A/E/I=1-95.
DR MGI; MGI:131327; Vamp2.
DR RGD; 3949; Vamp2.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; SYNAPTOBREVN; 1.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS50892; V-SNARE; 1.
DR 3D-structure; Acetylation; Coiled coil; Multigene family;
KM Polymorphism; Synapse; Synaptosome; Transmembrane.
FT INT MET 0 By similarity.
FT DOMAIN 1 93 Cytoplasmic (Potential).
FT TRANSMEM 94 113 Anchor for type IV membrane protein
FT 114 115 Vesicular (Potential).
FT MOD RES 1 115 N-acetylsuccinyl (By similarity).
FT DOMAIN 30 90 V-SNARE coiled-coil homology.
FT VARIANT 110 110 I -> II.
FT VARIANT 111 111 V -> I.
FT HELIX 28 87
SQ SEQUENCE 115 AA; 12559 MW; EA400D6291ABF0BC CRC64;
Query Match 81.9%; Score 181; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.8e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22386577; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klammer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshitoki S., Carranci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huylk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strusberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strusberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strusberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002737; AAH02737.3; -
DR EMBL; BC019608; AAH19608.1; -
DR EMBL; BC033870; AAH33870.1; -
DR HSSP; Q9WUM2; 1SFC.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; SYNAPTOBREVN; 1.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS50892; V-SNARE; 1.
SQ SEQUENCE 116 AA; 12663 MW; 9CD679CA6F1B5A8 CRC64;
Query Match 81.9%; Score 181; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.8e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
Q9BUC2 PRELIMINARY; PRT; 116 AA.
AC Q9BUC2;
DT 01-JUN-2001 (TRENBLREL 17, Created)
DT 01-JUN-2001 (TRENBLREL 17, Last sequence update)
DT 01-OCT-2004 (TRENBLREL 28, Last annotation update)
DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).
OS Name=VAMP2;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 7
Q9N0Y0 PRELIMINARY; PRT; 116 AA.
AC Q9N0Y0;
DT 01-OCT-2000 (TRENBLREL 15, Created)
DT 01-OCT-2000 (TRENBLREL 15, Last sequence update)
DT 01-JUN-2003 (TRENBLREL 24, Last annotation update)
DE VAMP-2.
OS Macaca mulatta (Rhesus macaque);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecinae; Macaca.
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RL Olsen S.K., Doerre S., Corley R.B.;
 DR Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF007168; AAB62931.1; -
 DR PIR; S3554; S3554.
 DR HSSP; O9WTW2; 1SFC.
 DR MGD; MGI:131277; Vamp2.
 DR GO; GO:0030141; C:secretory granule; IDA.
 DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.
 DR GO; GO:0042589; C:zymogen granule membrane; IDA.
 DR GO; GO:0005516; P:calmodulin binding; IDA.
 DR GO; GO:0005543; P:phospholipid binding; IDA.
 DR GO; GO:0000149; F:SNARE binding; IDA.
 DR GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.
 DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

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 RP SEQUENCE FROM N.A.
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 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
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 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

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 RN NCBI_TaxID=9544;
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 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
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 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
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 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
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 DR PROSITE; PS50892; V_SNAKE; 1.
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 RN NCBI_TaxID=9544;
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 RC TISSUE=Hippocampus;
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 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
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 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

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 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
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 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

OC
 RN NCBI_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RL Jensen M.J., Smith L.A.;
 DR Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF240769; AAF64476.1; -
 DR HSSP; O9WTW2; 1SFC.
 DR InterPro: IPR001388; Synaptoobrevin.
 DR Pfam; PF00957; Synaptoobrevin.1.
 DR PRINTS; PR00219; SYNAPTOBREVN.
 DR ProDom; PD001229; synaptoobrevin.1.
 DR PROSITE; PS00417; SYNAPTOBREVN.1.
 DR PROSITE; PS50892; V_SNAKE; 1.
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko U., Marinova K., Palmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi W.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWay P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting U., Madan A., Young A.C., Shevchenko Y., Bouffard G.O.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
 SEQUENCE FROM N.A.

RC TISSUE=Brain;
 RA Strausberg R.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC055105; AAH5105.1; 4A0D0D56B5409D0A CRC64;
 SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LSEIDRRADALQAGASOFETSAAKLRKRYWKXK 38
 60 LSEIDRRADALQAGASOFETSAAKLRKRYWKXK 94

RESULT 11
 BAC41125 PRELIMINARY; PRT; 116 AA.

AC BAC41125;
 DT 14-APR-2004 (TREMBLrel. 27, Created)
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DE 15 days embryo brain cDNA, RIKEN full-length enriched library,
 DE clone:G650012G02 product:unclassified, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RA 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RL Nature 409:685-690(2001).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [4]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RA MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=20530913; PubMed=1076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishi Y., Nakamura S., Hazama W., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirazane T.,
 RA Hori F., Imocani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takekura Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK090178; BAC41125.1; 4A0D0D56B5409D0A CRC64;
 SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LSEIDRRADALQAGASOFETSAAKLRKRYWKXK 38
 60 LSEIDRRADALQAGASOFETSAAKLRKRYWKXK 94

RESULT 12

Q9WUW2 PRELIMINARY; PRT; 135 AA.

AC Q9WUW2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-2003 (TREMBLrel. 24, Last annotation update)
 DE Vesicle associated membrane protein 2B.
 GN Name=Vamp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RC MEDLINE=99297576; PubMed=10371166;
 RA Mandic R., Lowe A.W.;
 RT "Characterization of an alternatively spliced isoform of rat vesicle
 RT associated membrane protein-2 (VAMP-2).";
 RL FEBS Lett. 451:209-213(1999).
 DR EMBL: AJ133104; CAB43509.1;
 DR InterPro: IPR001388; SynaptoCobrevin.
 DR Pfam: PF00957; SynaptoCobrevin; 1.
 DR PRINTS: PR00219; SYNAPTOCobrevin.
 DR ProDom: PD001229; SynaptoCobrevin; 1.

DR PROSITE: PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE: PS50892; V-SNARE; 1.
 SQ SEQUENCE 135 AA; 14509 MW; F37D14A87BDAB16 CRC64;
 Query Match 81.9%; Score 181; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 9.2e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYKWWKXNLK 38
 |||
 DB 60 LSELDPRADALQAGASQFETSAAKLKRYKWWKXNLK 94

RESULT 13
 ID Q8CHRA PRELIMINARY; PRT; 142 AA.
 AC Q8CHRA;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Vamp2 protein (Fragment).
 GN Name=Vamp2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22389257; PubMed=1247932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Ditchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 Kravitski M.I., Skalska U., Smaltz D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RU Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RU Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC039745; AA839745.1; -;
 DR HSSP; O9MTW2; ISFC.
 DR MGD; MGI:1313277; Vamp2.
 DR GO; GO:0030141; C:secretory granule; IDA.
 DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.
 DR GO; GO:0042589; C:zymogen granule membrane; IDA.
 DR GO; GO:0005516; F:calmodulin binding; IDA.
 DR GO; GO:0005543; F:phospholipid binding; IDA.
 DR GO; GO:0000149; F:SNARE binding; IDA.
 DR GO; GO:001155; P:calcium ion-dependent exocytosis; IDA.
 DR GO; GO:001157; P:regulation of exocytosis; IDA.
 DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.
 DR InterPro; IPR001388; SynaptoBrevin.
 DR Pfam; PF00957; SynaptoBrevin; 1.
 DR PRINTS; PR00219; SYNAPTOBREVIN.
 DR PRODOM; PD001229; SYNAPTOBREVIN.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS00417; SYNAPTOBREVIN; 1.
 DR PROSITE; PS50892; V-SNARE; 1.

FT NON TER 1 1
 SQ SEQUENCE 142 AA; 15313 MW; F1B0C9C9B495B76 CRC64;
 Query Match 81.9%; Score 181; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 9.7e-16;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYKWWKXNLK 38
 |||
 DB 86 LSELDPRADALQAGASQFETSAAKLKRYKWWKXNLK 120

RESULT 14
 ID VAM2_XENLA STANDARD; PRT; 113 AA.
 AC P47193;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoBrevin 2)
 DE (SYBII).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang X.-H., Poo M.-M.;
 RU Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 32-113 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=95324415; PubMed=7601005;
 RA Knecht A.K., Good P.J., David I.B., Harland R.M.;
 RT "Dorsal-ventral patterning and differentiation of noggin-induced
 RT neural tissue in the absence of mesoderm.";
 RL Development 121:1927-1935(1995).
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport
 CC vesicles to their target membrane.
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
 CC vesicles.
 CC -1- SIMILARITY: Belongs to the synaptoBrevin family.
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF035017; AAB88138.1; -;
 CC EMBL; U16801; AAB81376.1; -;
 CC HSSP; P19065; 1F83.
 CC InterPro; IPR001388; SynaptoBrevin.
 CC Pfam; PF00957; SynaptoBrevin; 1.
 CC PRINTS; PR00219; SYNAPTOBREVIN.
 CC PRODOM; PD001229; SYNAPTOBREVIN.
 CC PROSITE; PS00417; SYNAPTOBREVIN; 1.
 CC PROSITE; PS50892; V-SNARE; 1.
 CC Acetylation; Coiled coil; Multigene family; Synapse; Synaptosome;
 CC Transmembrane.
 CC INT MET 0
 CC TRANS MEM 92 110
 CC TRANS MEM 92 110
 CC DOMAIN 111 113
 CC MOD RES 1 1
 CC DOMAIN 28 88
 CC SEQUENCE 113 AA; 12341 MW; 6EC6C937B29BC6AB CRC64;

Query Match 81.0%; Score 179; DB 1; Length 113;
 Best Local Similarity 97.1%; Pred. No. 1,4e-15;
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 1, 2004, 17:59:10
 Job time : 117.625 secs

QY 4 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 38
 57 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 91

RESULT 15

AAH60344 PRELIMINARY; PRT; 114 AA.
 ID AAH60344;
 AC AAH60344;
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
 DE Vamp2-B-prov protein.
 GN VAMP2-B-PROV.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.U., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strusberg R.;
 RA Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC060344; AAH60344.1; -
 SQ SEQUENCE 114 AA; 12472 MW; AEF2EDCDP2D1DBF CRC64;

Query Match 81.0%; Score 179; DB 2; Length 114;
 Best Local Similarity 97.1%; Pred. No. 1,4e-15;
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 38
 58 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 92